

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 19:09:15 ; Search time 39 Seconds
(without alignments)
394.735 Million cell updates/sec

Title: US-10-816-698-3

Perfect score: 809

Sequence: 1 MSEVRPLSRDILMETLLYEQ.....LILLALLPLLSGGLHLILK 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	809	100.0	160	2 S58214	apoptosis inducer
2	97.5	12.1	509	2 G87596	cryptophan halogen
3	83.5	10.3	373	1 DERTH2	3beta-hydroxy-Delt
4	82	10.1	675	1 H69200	heavy-metal transp
5	81.5	10.1	373	1 DERTHM	3beta-hydroxy-Delt
6	81.5	10.1	635	2 S16567	beta-1,4-D-xylanas
7	80.5	10.0	633	2 S76749	hypothetical prote
8	78	9.6	431	2 S50633	hypothetical prote
9	77	9.5	1092	2 T12520	hypothetical prote
10	77	9.5	1173	2 H83189	DNA polymerase III
11	76.5	9.5	1004	1 S55353	probable copper-tr
12	76	9.4	406	2 B81391	zinc proteinase-li
13	75	9.3	320	2 S07384	diaminopimelate de
14	75	9.3	655	2 AD2422	DNA polymerase III
15	74.5	9.2	172	2 AF0109	flavodoxin 2 (impo
16	74.5	9.2	447	2 T46128	hypothetical prote
17	74	9.1	389	2 S38359	ribosomal protein
18	73.5	9.1	171	2 AE0350	conserved hypothet
19	73	9.0	404	2 A72496	hypothetical prote
20	72.5	9.0	321	2 T01521	syn-taxin homolog 1
21	72.5	9.0	490	2 E96010	probable two-compo
22	72.5	9.0	615	2 S82330	transcription init
23	72	8.9	1048	1 BVEGSC	exonuclease (EC 3.
24	71.5	8.8	343	2 C89779	hypothetical prote
25	71.5	8.8	389	2 E96498	L3 cytoplasmic rib
26	71.5	8.8	617	2 AF1284	5-methyltetrahydro
27	71.5	8.8	677	2 B71306	hypothetical prote
28	71.5	8.8	857	2 F84227	molybdenum-binding
29	71	8.8	217	2 B83643	conserved hypothet

30	71	8.8	322	2 F83300	probable enoyl-CoA
31	71	8.8	391	2 C71499	probable gen. secr
32	71	8.8	799	2 S55656	ribonucleoside-dip
33	71	8.8	1953	2 T40642	probable helicase
34	70.5	8.7	253	2 B69758	conserved hypothet
35	70.5	8.7	350	2 C83608	probable transcrip
36	70.5	8.7	390	2 C86641	60S ribosomal prot
37	70.5	8.7	390	2 C86641	ribosomal protein
38	70.5	8.7	390	2 J00772	phytochrome B - so
39	69.5	8.6	1156	2 T07756	hypothetical prote
40	69.5	8.6	188	2 T34881	phosphoglycerate d
41	69.5	8.6	525	2 H69229	sensory transduct
42	69.5	8.6	674	2 S75662	probable membrane
43	69.5	8.6	675	2 S59379	hypothetical prote
44	69.5	8.6	822	2 T00269	2-oxoglutarate deH
45	69	8.5	345	2 C72760	probable heme expo

ALIGNMENTS

RESULT 1

S58214

apoptosis inducer NBK - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S58214; G02437

R:Pun, K.T.; Farrow, S.N.; Raven, T.; Wride, C.J.; White, J.H.M.; Brown, R.

submitted to the EMBL Data Library, July 1995

A:Description: E1B-19K interacts with a novel apoptotic inducer, NBK.

A:Reference number: S58214

A:Accession: S58214

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-160 <PUN>

A:Cross-references: UNIPROT:Q13323; UNIPARC:UPI000000D929; EMBL:X89986; NID:g929654; PID:

R:Han, J.

submitted to the EMBL Data Library, February 1996

A:Reference number: H01273

A:Accession: G02437

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-160 <HAN>

A:Cross-references: UNIPARC:UPI000000D929; EMBL:U49730; NID:g1229145; PID:g1229146

C:Keywords: apoptosis

Query Match 100.0%; Score 809; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 9.9e-71;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

Db 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

QY 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120

Db 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120

QY 121 FWRSPNPGSVWVCEQVLLALLLALLLPLLSGGLHLILK 160

Db 121 FWRSPNPGSVWVCEQVLLALLLALLLPLLSGGLHLILK 160

RESULT 2

G87596

cryptophan halogenase, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87596

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Debois, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

RESULT 6

SI6567
beta-1,4-D-xylanase - Butyrivibrio fibrisolvens
C:Species: Butyrivibrio fibrisolvens
C>Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: SI6567
R:Lin, L.L.; Thomson, J.A.
Mol. Gen. Genet. 228, 55-61, 1991
A:Title: Cloning, sequencing and expression of a gene encoding a 73 kDa xylanase enzyme
A:Reference number: SI6567; MUID:91360090; PMID:1909424
A:Accession: SI6567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-635 <LIN>
A:Cross-references: UNIPROT:P26223; UNIPARC:UPI000013908D; EMBL:X61495; NID:948962; PIDN
A:Note: the authors translated the codon CTT for residue 131 as Asp and GAT for residue
F:30-338/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 10.1%; Score 81.5; DB 2; Length 635;
Best Local Similarity 25.0%; Pred. No. 7.1;
Matches 33; Conservative 28; Mismatches 48; Indels 23; Gaps 7;

QY 5 RPLSRDILMETLLYBOLLEPPTMEVLGMDTS--EDLDPMEDFDSLECMGSDALALRLA 62
DB 197 QWKEDFILEKVL-CPLDKLIDGKQSHLLMDHPDISEVRTALE-MYGSTGLQIHIT 254
QY 63 CIGDEMVSRLAPRLAQSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENI--MR 120
DB 255 ---ELDMHNADP-----SESMHALATRY-----QEPFQTYLDKSKGANITSVT 297
QY 121 FWRSPNPGSWVS 132
DB 298 FWNLLDENSWS 309

RESULT 7

S76749
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <KAN>
A:Cross-references: UNIPROT:P74554; UNIPARC:UPI00000C0E94; EMBL:D90916; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.0%; Score 80.5; DB 2; Length 633;
Best Local Similarity 23.8%; Pred. No. 8.8;
Matches 43; Conservative 26; Mismatches 45; Indels 67; Gaps 8;

QY 1 MBEVRPLSRDILMETLLYBOLLEPPTMEVLGMDTS--EDLDPMEDFDSLECMGSDAL 57
DB 120 LSVQVDRSQD-----TSEQILQ--AIAVLRTQVGNQSNLILDP--DLDSYYLME---AL 166
QY 58 ALR-----LACIG-----DEMDSRLAPRLAQSEVAMHSLGLAFIYDQ 96
DB 167 LKLPOLQTLAQGHIIIAHSGFGLSPAESQVLVIKLAQLKTSLVNGLVAETHA 226
QY 97 TEDIRDVLRSFMDGFTTLKE-----NIMRFRWSPN 126
DB 227 RQQLPRVINSGLNLTIVLEELFQSLTKVITGQIKLNDALNQCSQWGLLSLHFWRLVS 286

QY 127 P 127
DB 287 P 287

RESULT 8

S50633
hypothetical protein YER130c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C:Accession: S50633
R:Dieckrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda da
A:Reference number: S50437
A:Accession: S50633
A:Molecule type: DNA
A:Residues: 1-431 <DIE>
A:Cross-references: UNIPARC:UPI0000017CCA8; EMBL:U18916; GSPDB:GN000005; MIPS:YER130C
C:Genetics:
A:Gene: MIPS:YER130C
A:Cross-references: SGD:S00000932
A:Map position: 5R

Query Match 9.6%; Score 78; DB 2; Length 431;
Best Local Similarity 25.4%; Pred. No. 9.7;
Matches 35; Conservative 21; Mismatches 42; Indels 40; Gaps 7;

QY 28 EVLGWTDSEEDL---DPMEDFDSLECMGSDALALRLACIGDEMVSRLAPRLAQ----- 79
DB 103 EFFGRRELNEPLFNNDIVENDDDDIINNESDVLVMS-----DDELVNERFSLKQQLDG 158
QY 80 -----LSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTL---KENIMRFRW 123
DB 159 LNRISSTNVLKNLEIHE-----FIIDPTENIDDELE---DSFTTVPSQKKKVRDYFKLNIF 211
QY 124 -----SPNPGSWVSCEQV 136
DB 212 GSSSSSSNNNSNLGCEPI 229

RESULT 9

T12520
hypothetical protein DKFZp434G173.1 - human
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12520
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1092 <WAM>
A:Cross-references: UNIPARC:UPI00000711F2; EMBL:AL080133
A:Experimental source: adult testis; clone DKFZp434G173
C:Genetics:
A:Note: DKFZp434G173.1

Query Match 9.5%; Score 77; DB 2; Length 1092;
Best Local Similarity 24.8%; Pred. No. 36;
Matches 33; Conservative 22; Mismatches 44; Indels 34; Gaps 5;

QY 19 EQLLEPPTMEVLGMDTSIEDLDPMEDFDSLECMGSDALALRLACIGDEM--VSLRAPRL 77
DB 961 KQLREQVSQDLMALQGTQNPASPLPSFDEVDS-----GDQPPATSVAPRA 1006
QY 78 AOLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIM-RFWRSPNPGSWVSCEQV 136
DB 1007 KQFRAV-----RTTEGEETESRVFGSTPQRSFSLSRVRAALP-----LQL 1048
QY 137 LLALLLLALLLP 149
|| ||||| |||

Db 1049 LLLLLLLLLCLLP 1061

RESULT 10

H83189

DNA polymerase III, alpha chain PA3640 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: H83189

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bzadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latzbig, K.; Lim, J.; Lozy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

A:Reference number: A82950; MUID:2043737; PMID:10984043

A:Accession: H83189

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1173 <STO>

A:Cross-references: UNIPROT:Q9HXZ1, UNIPARC:UPI00001296DE, GB:AE004784; GB:AE004091; NID:10984043

C:Genetics:

C:Superfamily: DNA-directed DNA polymerase III alpha chain

Query Match 9.5%; Score 77; DB 2; Length 1173;

Best Local Similarity 25.2%; Pred. No. 40;

Matches 33; Conservative 21; Mismatches 33; Indels 44; Gaps 6;

Qy 1 MSEVRPLSRDILMETLAEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMEGSD----- 55

Db 377 ITDDIDPLAYD-----LIFERFLNERTS-----MPDFVDVFCNEGRDVIDY 418

Qy 56 -----ALALRLACIGDEMVDVSLRAPRLA-QLSEVAMHSIGLAF--IYD 95

Db 419 VADAVGRNAVQIITFTGTTAAK-AVRVDVARVQCKSYGLADRLSKMTIPFVGVGMDLTKAYE 477

Qy 96 QTEDIRDVLRS 106

Db 478 QEMLRDLFLKS 488

RESULT 11

S55353

probable copper-transporting ATPase (EC 3.6.1.-) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein P9954.6; protein YDR270w

C:Species: Saccharomyces cerevisiae

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004

C:Accession: S55353; S70129; S48298

R:Fu, D.; Beeler, T.J.; Dunn, T.M.

Yeast 11, 283-292, 1995

A:Title: Sequence, mapping and disruption of CCC2, a gene that cross-complements the Ca²⁺ requirement of yeast

A:Reference number: S55353; MUID:95304841; PMID:7785328

A:Accession: S55353

A:Molecule type: DNA

A:Residues: 1-1004 <FUD>

A:Cross-references: UNIPROT:P38995; UNIPARC:UPI000012663A; EMBL:L36317; NID:9538514; PID:10984043

R:Le, T.

submitted to the EMBL Data Library, May 1996

A:Description: The sequence of S. cerevisiae cosmid 9954.

A:Reference number: S70124

A:Accession: S70129

A:Molecule type: DNA

A:Residues: 1-1004 <LET>

A:Cross-references: UNIPARC:UPI000012663A; EMBL:U51030; NID:g1332633; PIDN:AAB64451.1; F:86-115/Domain: heavy-metal-associated homology <HMA1>

C:Genetics:

A:Gene: SGD:CCC2; MIPS:YDR270w

A:Cross-references: SGD:S0002678; MIPS:YDR270w

A:Map position: 4R

C:Superfamily: yeast copper-transporting ATPase; ATPase nucleotide-binding domain homology <HMA1>

C:Keywords: ATP; copper transport; hydrolase; ion transport; metal binding; transmembrane protein

F:86-115/Domain: heavy-metal-associated homology <HMA1>

F:262-278/Domain: transmembrane #status predicted <TM1>

F:304-320/Domain: transmembrane #status predicted <TM2>

F:308-376/Domain: ATPase transduction domain homology <ATT>

F:340-356/Domain: transmembrane #status predicted <TM3>

F:533-549/Domain: transmembrane #status predicted <TM4>

F:574-590/Domain: transmembrane #status predicted <TM5>

F:757-909/Domain: ATPase nucleotide-binding domain homology <ATN>

F:905-921/Domain: transmembrane #status predicted <TM6>

F:934-950/Domain: transmembrane #status predicted <TM7>

F:11,13,16/Binding site: copper (Met, Cys, Cys) #status predicted

F:89,91,94/Binding site: copper (Met, Cys, Cys) #status predicted

Query Match 9.5%; Score 76.5; DB 1; Length 1004;

Best Local Similarity 23.08; Pred. No. 37;

Matches 37; Conservative 33; Mismatches 38; Indels 53; Gaps 9;

Qy 33 TDSIEDLDPMED--FDSLECMEGS-----DALALRLACIGDE---- 67

Db 129 TLTETAREMIEDCGFDSNIIMDGNADMTKTVLKVKAFEDSEPLILSSVSERFOFL 188

Qy 68 MDVSLRAPRLAQLSEVAMHSIGLAFIYDQTEIRDLRL-----SFMGDFITL- 114

Db 189 LDGKVKSIISD---DMHTLTIKYCCNEL-GIRDLRLHLRTGYKTFVSNLNDTTLQLR 243

Qy 115 ---KENIMRFRSPNPGSVSWSCQVLLALL-LIALLLPLL 151

Db 244 LLSKEDIRFWKKN-----SIKSTLLAIICMLLYMIVPM 278

RESULT 12

B81391

zinc proteinase-like protein Cj0463 [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: B81391

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, C.W.; Quail, M.; Rajadaram, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell, A.; et al.

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervirulence

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: B81391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <PAR>

A:Cross-references: UNIPROT:Q9PI45; UNIPARC:UPI000000C213D; GB:AL1139075; GB:AL111168; NID:10688204

C:Genetics:

A:Gene: Cj0463

Query Match 9.4%; Score 76; DB 2; Length 406;

Best Local Similarity 23.5%; Pred. No. 14;

Matches 31; Conservative 28; Mismatches 37; Indels 36; Gaps 5;

Qy 47 SLECMEGSDALALRLACIGDEMVDVSLRA-----PRLAQ--LSEVAMHSIGLAFIYDQT 97

Db 69 NLEASSGFESLEINSLCNFNDFALKSLKLEKLLKPRIEKTLOKLKINALG----- 120

Qy 98 EDIRDLVRSFMDGFTTKENIM-----RPWRSPNPGSVSWSCQVLLALL-----LL 143

Db 121 -----ELASKNSDPDYLAKNLLNAQIFKCKEFQSPNDGDEKSIETLSLKDLOQNFYKNFIH 175

Qy 144 LALLPLLSGGL 155

Db 176 LSDLVILGGDL 187

RESULT 13

S07384

diaminopimelate dehydrogenase (EC 1.4.1.16) - Corynebacterium glutamicum

C:Species: Corynebacterium glutamicum

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: S07384

R:Ishino, S.; Mizukami, T.; Yamaguchi, K.; Katsumata, R.; Araki, K.

Nucleic Acids Res. 15, 3917, 1987
 A:Title: Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium
 A:Reference number: S07384; MUID:87231077; PMID:3588313
 A:Accession: S07384
 A:Molecule type: DNA
 A:Residues: 1-320 <ISH>
 C:Genetics: UNIPROT:P04964; UNIPARC:UPI000003ABB7; EMBL:Y00151; NID:g40492; PIDN:BA000001
 A:Gene: ddh
 C:Keywords: NADP; oxidoreductase

Query Match 9.3%; Score 75; DB 2; Length 320;
 Best Local Similarity 24.1%; Pred. No. 13;
 Matches 32; Conservative 25; Mismatches 59; Indels 18; Gaps 5;
 QY 13 METLLYEQLLEPPPTMEVLGMDTSEEDLDPMED-FDSLECMGSDALALRLACIGDEMDVS 71
 DB 18 VEKLIKQ-----PMDLVGIFSRATLTCTKPFVDVADVDKHAADDVDVFLCMGSAITDIP 73
 QY 72 LRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDV--LRSPMDGFTTLKENIMRFRSPNPGS 129
 DB 74 EOAPKFAQ-----FACTVDYDNRDIPRHRQVMEANAAAGNVALVSTGWDFQM 123
 QY 130 WVSCEQVLLALLL 142
 DB 124 P-SINRVYAAAVL 135

RESULT 14
 AD2422
 DNA polymerase III gamma and tau chains [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AD2422
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-655 <KUR>
 A:Cross-references: UNIPROT:Q8YMK1; UNIPARC:UPI00000CECD5; GB:BA0000019; PIDN:BA076631.1;
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4932

Query Match 9.3%; Score 75; DB 2; Length 655;
 Best Local Similarity 24.6%; Pred. No. 31;
 Matches 49; Conservative 25; Mismatches 63; Indels 62; Gaps 10;
 QY 17 LYEQLLEPP--TMEVLGMDTSEEDLDP-----EDFDSLECMGSDALALRLACIG--D 66
 DB 141 LUKTLEPPRHVVFLATDIPORVLTISRCQRFDRFRIQL-----EAMVKHLSAISKE 196
 QY 67 ENDVSLRAPRL--AQLS-----EVAMHSLGL-----A 91
 DB 197 NINISLEAVTLVAQLSQGLRDAESLDDQLALLPNEVTPQVMDLVGVSVEQDLVLLAA 256
 QY 92 FYDQTEDIRDLVRSFMDGF--TTLKENIMRFR-----SPNPGSWVSCEQVLLALL 141
 DB 257 IAQDNPELVLDSTQRLDREGREPLTILQNLAAFYRDLIAKTAAPNRHNLVACTQOTWKAL 316
 QY 142 LLLALLLP--LLSGGLHL 157
 DB 317 VESAQSLPISTILLGQKHL 335

RESULT 15
 AF0109
 Flavodoxin 2 [imported] - Yersinia pestis (strain C092)

C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AF0109
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Eil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I.
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 <KUR>
 A:Cross-references: UNIPROT:Q8ZHKO; UNIPARC:UPI00000CD761; GB:AL590842; PIDN:CAC89737.1;
 C:Genetics:
 A:Gene: fldB
 C:Superfamily: flavodoxin; flavodoxin homology
 C:Keywords: flavoprotein

Query Match 9.2%; Score 74.5; DB 2; Length 172;
 Best Local Similarity 24.9%; Pred. No. 7.2;
 Matches 45; Conservative 18; Mismatches 43; Indels 75; Gaps 9;
 QY 9 RDILMETL-----LYEQLLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 DB 22 RDILGEDLVLDLHNLKEVSPRLMEYSILILGI-----PTWDFGELQ--EDWEAI--- 68
 QY 61 LACIGDEMDVSLRAPRLAQLS-----EVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKE 116
 DB 69 -----WPQTLQNLKGIKIVAMYGMDQFGY--SEWFLDALGMLHDHTAPLGV 113
 QY 117 NIMRFR-----RSPNPGS-----WVSCEQVLLALLL 143
 DB 114 KFIGFWPTDGFETTSKPLSADGKQFVGLALDEVNQVLDSEIRIQW--CEQILMEAL 171
 QY 144 L 144
 DB 172 L 172

Search completed: March 15, 2006, 19:13:34
 Job time : 41 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 19:05:54 ; Search time 229 Seconds
(without alignments)
492.946 Million cell updates/sec

Title: US-10-816-698-3

Perfect score: 809

Sequence: 1 MSEVRPLSRDILMETLLEQ.....LLLLALLPLSLGGHLHLK 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809	100.0	160	1 BIK HUMAN	Q13323 homo sapien
2	809	100.0	160	2 Q6FH93 HUMAN	Q6FH93 homo sapien
3	301	37.2	158	2 Q925D2 RAT	Q925D2 rattus norv
4	291	36.0	158	2 Q99L97 MOUSE	Q99L97 mus musculu
5	284	35.1	150	2 Q70337 MOUSE	Q70337 mus musculu
6	97.5	12.1	509	2 Q9A4M3 CAUCR	Q9A4M3 caulobacter
7	94.5	11.7	678	2 Q72WM4 DESVH	Q72WM4 desulfovibr
8	85.5	10.6	405	2 Q7PK12 ANOGA	Q7PK12 anopheles g
9	85	10.5	2004	2 Q4WGN9 ASPFU	Q4WGN9 aspergillus
10	84.5	10.4	705	2 Q70C70 STRTR	Q70C70 streptococc
11	84	10.4	1120	2 Q9VUK6 DROME	Q9VUK6 drosophila
12	84	10.4	2726	2 Q6UBD8 DROME	Q6UBD8 drosophila
13	83.5	10.3	265	1 CAD10 MOUSE	P70408 mus musculu
14	83.5	10.3	329	2 Q7PD23 GIALA	P70408 mus musculu
15	83.5	10.3	372	1 3BHS2 RAT	P22072 r 3 beca-hy
16	82.5	10.2	167	2 Q5P8D1 AZOSE	Q5P8D1 azoarcus sp
17	82.5	10.2	705	2 Q4KTJ3 LACT	Q4KTJ3 lactococcus
18	82.5	10.2	705	2 Q4LENI LACTC	Q4LENI lactococcus
19	82.5	10.2	705	2 P948B8 LACTC	P948B8 lactococcus
20	82.5	10.2	705	2 Q9FBF7 LACTA	Q9FBF7 lactococcus
21	82.5	10.2	705	2 Q7AY49 STRTR	Q7AY49 streptococc
22	82.5	10.2	705	2 Q926K0 LISTIN	Q926K0 listeria in
23	82.5	10.2	964	2 Q9NV77 HUMAN	Q9NV77 homo sapien
24	82.5	10.2	1045	2 Q9NVW1 HUMAN	Q9NVW1 homo sapien
25	82.5	10.2	1769	2 Q9P273 HUMAN	Q9P273 homo sapien
26	82.5	10.2	1828	2 Q80TD2 MOUSE	Q80TD2 mus musculu
27	82.5	10.2	2346	2 Q9JLC1 MOUSE	Q9JLC1 mus musculu
28	82.5	10.2	2715	2 Q9WTS6 MOUSE	Q9WTS6 mus musculu
29	82	10.1	675	2 Q26849 METHH	Q26849 methanobact
30	82	10.1	1199	2 Q7UUS6 RHOPA	Q7UUS6 rhodospirell
31	81.5	10.1	247	2 Q4RUG4 TETNG	Q4RUG4 tetraodon n

32 81.5 10.1 635 1 XYNB_BUTFI
33 81.5 10.1 806 2 Q5UWB2 HALMA
34 81.5 10.1 1710 2 Q6FPU9 CANGA
35 80.5 10.0 633 2 P74554 SYNY3
36 80.5 10.0 732 2 Q4SENO TETNG
37 80 9.9 352 2 Q5FFV9 BHRRG
38 80 9.9 352 2 Q5FD77 EHRRW
39 80 9.9 352 2 Q5HAF9 EHRRW
40 80 9.9 1928 2 Q5GA85 RHAB
41 79.5 9.8 444 2 Q8TX27 METKA
42 79.5 9.8 809 2 Q2TJ36 TET2
43 79.5 9.8 1390 2 Q5THB6 PYRKO
44 79 9.8 204 2 Q6GZXO FRG3V
45 79 9.8 278 2 Q5Y3QI_9NEOP

ALIGNMENTS

RESULT 1
BIK_HUMAN
ID BIK_HUMAN STANDARD; PRT; 160 AA.
AC Q13323; Q16582;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Bcl-2 interacting killer (Apoptosis inducer NBK) (BP4) (BIPI1).
GN Name=BIK; Synonyms=NBK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B-cell;
RX MEDLINE=96068922; PubMed=7478623;
RA Boyd J.M., Gallo G.J., Elangovan B., Houghton A.B., Malstrom S.,
RA Avery B.J., Ebb R.G., Subramanian T., Chittenden T., Lutz R.J.,
RA Chinnadurai G.
RT "Bik, a novel death-inducing protein shares a distinct sequence motif
with Bcl-2 family proteins and interacts with viral and cellular
survival-promoting proteins.";
RL Oncogene 11:1921-1928(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96413338; PubMed=8816500;
RA Han J., Sabbatini P., White E.;
RT "Induction of apoptosis by human Nbk/Bik, a BH3-containing protein
that interacts with B1B 19K.";
RL Mol. Cell. Biol. 16:5857-5864(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Lymphoid;
RA Pun K.-T., Farrow S.N., Raven T., Wride C.J., White J.H.M., Brown R.;
RT "B1B-19K interacts with a novel apoptotic inducer, NBK.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=99431905; PubMed=10500065;
RA Castellis A., Inc Y., Louis D.N., Ramesh V., Gusella J.F., Rustgi A.K.;
RT "Mapping of a target region of allelic loss to a 0.5-cM interval on
chromosome 22q13 in human colorectal cancer.";
RL Gastroenterology 117:831-837(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed15461802; DOI=10.1186/gb-2004-5-10-x84;
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,
RA Coie C.G., Goward M.E., Aguado B., Malliya M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.;
RT "A genome annotation-driven approach to cloning the human ORFeome.";
RN Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).
[7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA]
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NTEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA [URL: <http://egp.gs.washington.edu>].";
RL Submitted (FEB-2003) to the ENBL/GenBank/DBJ databases.
[8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fay J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.P., Leverhwa M.A., Lloyd C., Lloyd D.M.,
RA Martyn J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Soderlund C., Spragon L., Steward C.A., Suleston J.E., Swann R.M.,
RA Vaubin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Asakaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malay E., Nguyen T., Pan H.,
RA Phan Q., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky J., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumaniski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
[9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.M., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlynski S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[10]
RP MUTAGENESIS, AND FUNCTION OF BH3 MOTIF.
RX MEDLINE=96091131; PubMed=8521816;
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell
death and protein binding functions.";
RL EMBO J. 14:5589-5596(1995).
CC -!- FUNCTION: Accelerates programmed cell death. Binding to the
apoptosis repressors Bcl-X(L), BHRFL, Bcl-2 or its adenovirus
homolog B19 protein suppresses this death-promoting activity.
CC Does not interact with BAX.
CC -!- SUBCELLULAR LOCATION: Around the nuclear envelope, and in
cytoplasmic membranes.
CC -!- DOMAIN: Intact BH3 motif is required by BIK, BID, BAK, BAD and BAX
for their pro-apoptotic activity and for their interaction with
anti-apoptotic members of the Bcl-2 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
EMBL; U34584; AAC50413.1; -; mRNA.
EMBL; U49730; AAC79124.1; -; mRNA.
EMBL; X89986; CAA62013.1; -; mRNA.
EMBL; AF174424; AAF01156.1; -; Genomic_DNA.
EMBL; AF174421; AAF01156.1; JOINED; Genomic_DNA.
EMBL; AF174422; AAF01156.1; JOINED; Genomic_DNA.
EMBL; AF174423; AAF01156.1; JOINED; Genomic_DNA.
EMBL; BT006728; AAF53374.1; -; mRNA.
EMBL; CR456390; CAG30276.1; -; mRNA.
EMBL; AY245248; AAO61089.1; -; Genomic_DNA.
EMBL; AL022237; CAA18260.2; -; Genomic_DNA.
EMBL; BC001599; AAH01599.1; -; mRNA.
PIR; S58214; S58214.
Ensembl; ENSG00000100290; Homo sapiens.
HGNC; HGNC:1051; BIK.
H-InvDB; HIX001651; -.
MIM; 603392; -.
GO; GO:0008632; P:apoptotic program; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
InterPro; IPR00712; Bcl2_BH.
PROSITE; PS01259; BH3; 1.
Kw Apoptosis; Transmembrane.
TRANSMEM; 136 156
FT DOMAIN 137 158
FT MOTIF 57 71
FT CONFLICT 149 150 PL -> LP (in Ref. 1).
FT SEQUENCE 160 AA; 18016 MW; 89034f443f5a136 CRC64;
Query Match 100.0%; Score 809; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 8.9e-70;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSEVRPLSRDILMETLLTLLYEQLEPPTEVLGVTMDSEDLDFMEDFDSLECNESDALAIR 60
Db 1 MSEVRPLSRDILMETLLTLLYEQLEPPTEVLGVTMDSEDLDFMEDFDSLECNESDALAIR 60
Qy 61 LACIGDEMDSVLSRAPRLAQLSEVAMHSIGLAFLYDQTEDIRDLVRSFMDGFTTLKENIMR 120

Db 61 LACIGDMDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGHLHLK 160

RESULT 2
ID Q6FH93 HUMAN PRELIMINARY; PRT; 160 AA.
AC Q6FH93;
DT 10-MAY-2005 (TREMELrel. 30, Created)
DT 10-MAY-2005 (TREMELrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
DE Bik protein.
GN Name=Bik;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541863; CAG46661.1; -; mRNA.
DR EMBL; CR541883; CAG46681.1; -; mRNA.
SQ SEQUENCE 160 AA; 18016 MW; 89034F4443F5A136 CRC64;

Query Match 100.0%; Score 809; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 8.9e-70;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDMDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
DB 61 LACIGDMDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGHLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGHLHLK 160

RESULT 3
ID Q925D2 RAT PRELIMINARY; PRT; 158 AA.
AC Q925D2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Bcl2-interacting killer-like protein.
GN Name=Bikl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=Sprague-Dawley.
RX MEDLINE=22672518; PubMed=12787069;
RA DOI=10.1046/j.1471-4159.2003.01795.x;
RA Itoh T., Itoh A., Pleasure D.,
RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation."
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AF372501; AAK53820.1; -; mRNA.

DR Ensembl; ENSRNOG00000010359; Rattus norvegicus.
DR RGD; 621547; Bikl.
SQ SEQUENCE 158 AA; 17660 MW; A637425508879C78 CRC64;
Query Match 37.2%; Score 301; DB 2; Length 158;
Best Local Similarity 44.3%; Pred. No. 8.4e-21;
Matches 74; Conservative 29; Mismatches 48; Indels 16; Gaps 7;
QY 1 MSEVPLSRDILMETLLYEQLLEP-----PTM-EVLGMDTSEEDLDPMEDFDSLECMG 53
DB 1 MSEARLMARDII-KTLLHDQVPQAVVSGAFSMKEPGV-----EDVSPVRLDFMRCL 55
QY 54 SDALALRLACIGDMDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTT 113
DB 56 RNOVALRLACIGDMDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTT 112
QY 114 LKENIMFWRSPNPGSWVSCQVLLALLLALLPLLSGGHLHLK 160
DB 113 LRENISW-WRVFTPGAWVSPDQFQPFPMVLLVFLLLGGAWHLQLQ 158

RESULT 4
Q99L97 MOUSE
ID Q99L97 MOUSE PRELIMINARY; PRT; 158 AA.
AC Q99L97;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Bikl protein.
GN Name=Bikl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX Strausberg R.,
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003732; AAH03732.1; -; mRNA.
DR Ensembl; ENSMUSG00000016758; Mus musculus.
DR MGI; MGI:1206591; Bikl.
DR GO; GO:0005740; C:mitochondrial membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
SQ SEQUENCE 158 AA; 17668 MW; D6483418215ABA48 CRC64;

Query Match 36.0%; Score 291; DB 2; Length 158;
Best Local Similarity 42.3%; Pred. No. 7.8e-20;
Matches 69; Conservative 34; Mismatches 52; Indels 8; Gaps 6;
QY 1 MSEVRPLSRDILMETLLYEQLLEPP-TMEVLGWTD--SEEDLDPMEDPDSLECMGSDAL 57
DB 1 MSEARLMARDVI-KTVPHDQVPPVASETSMKEPVAGENLSPRVDVLMCEVGRNQV 59
QY 58 ALRLACIGDMVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKEN 117
DB 60 ALRLACIGDMDCLSRPLVQLPGIAIHR--LAVTYSRT-GVRGIFRSIRSLTNLREN 116
QY 118 IMRFWRSPNPGSWSCQVLLALLLALLPLLSGGHLHLK 160
DB 117 IWS-WRVLTGAWVSPDQPGOLFPMVLLVFLLLGGAWYLQ 158
RESULT 5
O70337 MOUSE
ID O70337_MOUSE PRELIMINARY; PRT; 150 AA.
AC O70337;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Bik-like killer protein.
GN Name=Biklik; Synonyms=Bik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP "Bik, a BH3-containing mouse protein that interacts with Bcl-2 and Bcl-xL, is a potent death agonist."
RL J. Biol. Chem. 273:7783-7786(1998).
DR EMBL; AF048838; AAC40079.1; -; mRNA.
DR Ensembl; ENSMUSG0000016758; Mus musculus.
DR MGI; MGI:1206591; Biklik.
DR GO; GO:0005740; C:mitochondrial membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
SQ SEQUENCE 150 AA; 16901 MW; 120CB6BAA4612788 CRC64;
Query Match 35.1%; Score 284; DB 2; Length 150;
Best Local Similarity 42.5%; Pred. No. 3.5e-19;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;
QY 1 MSEVRPLSRDILMETLLYEQLLEPP-TMEVLGWTDSEEDLDPMEDPDSLECMGSDAL 60
DB 1 MSEARLMARDVI-KTVPHDQVPP--VASSTPSMK--EPVRDVLMECEVGRNQVALR 54
QY 61 LACIGDMVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKEN 120
DB 55 LACIGDMDCLSRPLVQLPGIAIHR--LAVTYSRT-GVRGIFRSIRSLTNLREN 111
QY 121 FWRSPNPGSWSCQVLLALLLALLPLLSGGHLHLK 160
DB 112 -WRVLTGAWVSPDQPGOLFPMVLLVFLLLGGAWYLQ 150
RESULT 6
Q9A4W3 CAUCR
ID Q9A4W3_CAUCR PRELIMINARY; PRT; 509 AA.
AC Q9A4W3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tryptophan halogenase, putative.

OrderedLocusNames=CC2807;
GN Caulobacter crescentus.
OS Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Eisen W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Niesen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A.S., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005946; AAK24771.1; -; Genomic_DNA.
DR PIR; G87596; G87596.
DR TIGR; CC2807; -.
DR InterPro; IPR006905; Trp_halogenase.
DR Pfam; PF04820; Trp_halogenase; 1.
KW Complete proteome.
SQ SEQUENCE 509 AA; 56072 MW; 6BA10B9F280C960D CRC64;
Query Match 12.1%; Score 97.5; DB 2; Length 509;
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 40; Conservative 26; Mismatches 78; Indels 19; Gaps 6;
QY 1 MSEVRPLSRDILMETLLYEQLLEPP-TMEVLGWTDSEEDLDPMEDPDSLECMGSDAL 60
DB 203 LEDGRVLEADLVDCSGFGLLIETQLQA-GYDDWSHWL-PNDRAVAMPCTVGGDLTPY 260
QY 61 LACIGDMVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDV-----LRSPMDGFTTLK 115
DB 261 TRATADAAGWRWRIP-----LQHTGNGYVY-SSRDISDEDAVARLRLTLDGEPLAE 311
QY 116 ENIMRFRWRSPNPGSWSCQVLLALLLALLPLLSGGHLHL 158
DB 312 PNFLRFQAGRKAQWV---KNVVAIGLSGFGFLEPLETSIH 351
RESULT 7
Q72WM4 DESVH
ID Q72WM4_DESVH PRELIMINARY; PRT; 678 AA.
AC Q72WM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Sensor histidine kinase.
GN OrderedLocusNames=DVUA0065;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feidblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AE017286; AAS94390.1; -; Genomic_DNA.

TIGR; DVUA0065; --
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005301; F:kinase activity; IEA.
 DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR003661; His_kinase.
 DR InterPro; IPR004358; His_kin_like_C.
 DR Pfam; PF02518; HisPase_C; 1.
 DR Pfam; PF00512; HisKA; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR SMART; SM00387; HATPase_C; 1.
 DR PROSITE; PS0109; HIS_KIN; 1.
 DR Complete proteome; Kinase; Pfamid.
 SK SEQUENCE 678 AA; 73820 MW; 240FED7865FC3263 CRC64;
 Query Match 11.7%; Score 94.5; DB 2; Length 678;
 Best Local Similarity 26.9%; Pred. No. 3.8; Mismatches 22; Indels 13; Gaps 3;
 Matches 28; Conservative 22; Mismatches 41; Indels 13; Gaps 3;
 QY 34 DSEDLDPWFDSLECMGSDALALRLACIGDEMVSRLAPRLAQLSEVAMHSL----- 88
 Db 431 DTREHD-LEDFELLEAMGRQIALCVSRFLGDELAVAREMEALGRFAALVNHDLKNQVY 489
 QY 89 GLAFIYD-----QTEDIRVLRSMFMDGFTTLKENIMRFRWSP 125
 Db 490 ALSLLVDNARLYIAEPEFQDLVETLTNSVSNMRNLISQLTRLP 533
 RESULT 8
 ID Q7PK12 ANOXA PRELIMINARY; PRT; 405 AA.
 AC Q7PK12
 DT 01-WAR-2004 (TREMBLrel. 26, Created)
 DT 01-WAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENSANGP0000024055.
 GN ORFNames=ENSANG0000024055;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC NUCLEOTIDE SEQUENCE.
 DR EMBL; AAB01008987; EAA43249.1; --; Genomic DNA.
 DR InterPro; IPR002016; Peroxidase.
 DR PROSITE; PS00436; PEROXIDASE 2; UNKNOWN 1.
 SQ SEQUENCE 405 AA; 47052 MW; 1B34C60EE72D877C CRC64;
 Query Match 10.6%; Score 85.5; DB 2; Length 405;
 Best Local Similarity 25.0%; Pred. No. 15; Mismatches 21; Indels 31; Gaps 4;
 Matches 29; Conservative 21; Mismatches 35; Indels 31; Gaps 4;
 QY 54 SPALALRLACIGDEMVSRLAPRLAQLS-----EVAMHSLGLAFIYDQTEIRDLV 104
 Db 45 SHALATLLCVYVVVILLTGIRYKPLTVNVLVWQCSSLHYVNLALIVYHLLPARPVI 104
 QY 105 RSMFMDGFTTL-----KENIMRFRWSPNPGSWVSCQVLLALLL 143
 Db 105 RNIFNGFVQLFRTLNGAGCHRWKGTCKXNVLK-----ALKMILCDTLTLCALFVL 155
 RESULT 9

Q4WGN9 ASPFU PRELIMINARY; PRT; 2004 AA.
 ID Q4WGN9
 AC Q4WGN9
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Guanylyl-nucleotide exchange factor (Sec7), putative.
 GN ORFNames=Afu7G05700;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyina I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares J.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT Aspergillus fumigatus";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC SEQUENCE 2004 AA; 225549 MW; 985CE30E0BA92457 CRC64;
 DR EMBL; AAF01000009; EAL86902.1; --; Genomic DNA.
 Query Match 10.5%; Score 85; DB 2; Length 2004;
 Best Local Similarity 29.0%; Pred. No. 1.1e+02;
 Matches 31; Conservative 19; Mismatches 41; Indels 16; Gaps 5;
 QY 41 PMEDFDSLE----CMGSDALALRLACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQ 96
 Db 1093 PMQDTQNLTTKLCMEGM-KLAIRISCAFD-----LETFRVAFVTGLAKFT-NLGNVREM 1145
 QY 97 TEDIRDVLRSMFMDGFTTLKENIMRFRWSPNPGSWVSCQVLLALLL 143
 Db 1146 VPKNVKALKALDVALTEGNNLKSSWREV-----LTCVSQDLRLQLL 1187
 RESULT 10
 ID Q70C70 STRTR PRELIMINARY; PRT; 705 AA.
 AC Q70C70
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Cadmium efflux ATPase.
 GN Name=cadA;
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1308;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CNR2308;
 RA Pavlovic G., Burrus V., Gintz B., Decaris B., Guedon G.;

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
 RA Hoskins R., Stapleton M., Facileb J., Park S., Svirskaas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003532; AAF49670.1; -; Genomic DNA.
 DR Ensembl; CG13459; Drosophila melanogaster.
 DR FlyBase; FBgn0036472; CG6735.
 DR FlyBase; FBgn0036472; CP309.
 SQ SEQUENCE 1120 AA; 124267 MW; 3060369B771168B6 CRC64;
 Query Match 10.4%; Score 84; DB 2; Length 1120;
 Best Local Similarity 27.8%; Pred. No. 71;
 Matches 32; Conservative 18; Mismatches 43; Indels 22; Gaps 4;
 QY 17 LYEQLLEPTMEVLGWTDSSEDLDPWDFSLCEMGSDALALRLACIGDMVSLRAPR 76
 DB 473 LQADVLEPLRLTLEMDDEEDDDSSQLAK-----LRLMANNQMIVD-NAPK 525
 QY 77 L-----AQLSEVAMHSLGL-----AFYDQTEDIRDLVRSFMDGFTTLKE 116
 DB 526 LSPTAEATQVTSNNLEIKQMRVPLTEFSKDVLEITESEERLLSMSTTME 580
 RESULT 12
 Q6UBD8 DROME PRELIMINARY; PRT; 2726 AA.
 AC Q6UBD8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 309 kDa centrosomal protein.
 GN Name=cp309;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14565985; DOI=10.1091/mbc.E03-03-0191;
 RA Kawaguchi S., Zheng Y.;
 RT "Characterization of a Drosophila centrosome protein CP309 that shares
 RT homology with Kendrin and CG-NAP."
 RL Mol. Biol. Cell 15:37-45(2004).
 DR EMBL; AV373570; AAR20251.1; -; mRNA.
 SQ SEQUENCE 2726 AA; 309269 MW; 219693735BCA070E CRC64;
 Query Match 10.4%; Score 84; DB 2; Length 2726;
 Best Local Similarity 27.8%; Pred. No. 2e+02;
 Matches 32; Conservative 18; Mismatches 43; Indels 22; Gaps 4;
 QY 17 LYEQLLEPTMEVLGWTDSSEDLDPWDFSLCEMGSDALALRLACIGDMVSLRAPR 76
 DB 302 LQADVLEPLRLTLEMDDEEDDDSSQLAK-----LRLMANNQMIVD-NAPK 354
 QY 77 L-----AQLSEVAMHSLGL-----AFYDQTEDIRDLVRSFMDGFTTLKE 116
 DB 355 LSPTAEATQVTSNNLEIKQMRVPLTEFSKDVLEITESEERLLSMSTTME 409

RESULT 13
 CAD10 MOUSE STANDARD; PRT; 265 AA.
 ID CAD10 MOUSE
 AC P70408;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cadherin-10 (T2-cadherin) (Fragment).
 GN Name=Cdh10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction."
 RL Biol. Reprod. 55:822-827(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 117-203.
 RC STRAIN=CBA/J; TISSUE=Thymocyte;
 RX MEDLINE=96211873; PubMed=8620560; DOI=10.1006/cimm.1996.0123;
 RA Munro S.B., Duclos A.J., Jackson A.R., Baines M.G., Blaschuk O.W.;
 RT "Characterization of cadherins expressed by murine thymocytes."
 RL Cell. Immunol. 169:309-312(1996).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- DEVELOPMENTAL STAGE: Expressed at all stages of testicular
 CC development with highest levels found in fetal gonad.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U69137; AAB87708.1; -; mRNA.
 CC Ensembl; ENSMUSG0000022321; Mus musculus.
 CC MGI; MGI:107436; Cdh10.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR00233; Cadherin_C_term.
 CC Pfam; PF01049; Cadherin_C; 1.
 CC SMART; SM00112; CA; 1.
 CC PROSITE; PS00232; CADHERIN_1; PARTIAL.
 CC PROSITE; PS0268; CADHERIN_2; 1.
 CC Calcium; Cell adhesion; Glycoprotein; Transmembrane.
 FT TOPO_DOM <1 96 Extracellular (Potential).
 FT TRANSMEM 97 117 Potential.
 FT TOPO_DOM 118 265 Cytoplasmic (Potential).
 FT DOMAIN <1 90 Cadherin 5.
 FT CARBOHYD 18 18 N-linked (GlcNAc...) (Potential).
 FT NON TER 1 1
 SQ SEQUENCE 265 AA; 29351 MW; 49A15B6C158C5503 CRC64;
 Query Match 10.3%; Score 83.5; DB 1; Length 265;
 Best Local Similarity 33.7%; Pred. No. 15;
 Matches 34; Conservative 12; Mismatches 30; Indels 25; Gaps 6;
 QY 3 EVPLSRDILMETLLYQLLEPTMEVLGWTDSSEDLDPWDFSLCEMGSDALALRLACIGDMVSLRAPR 83
 DB 160 EKKLRDRIPELFT-----PRTPTAGNTDVRDINERLKEHLDPTAPPYDSLATYA 214
 QY 51 MEGSDALALRLACI-----GDMVSLR--APRLAQLSEV 83

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Db 215 YEGNDSVAESLSLESQTTEGQNDYDLREWGPRPKLAEM 255
RESULT 14
ID Q7PD23 GIALA PRELIMINARY; PRT; 329 AA.
AC Q7PD23
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE GLP 474 749 1738 (GLP 149 7412 6423).
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]_TaxID=184922;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACB01000186; EAA36684.1; -; Genomic DNA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR PROSITE; PS50053; UBIQUITIN 2; 1.
SQ SEQUENCE 329 AA; 36491 MW; 7CB1ECBCC87A8CC7 CRC64;

Query Match 10.3%; Score 83.5; DB 2; Length 329;
Best Local Similarity 25.0%; Pred.No. 19;
Matches 49; Conservative 34; Mismatches 54; Indels 59; Gaps 12;

QY 10 DILMETLLEYQ-----LLE-PPTMEVLGMT-----DSEDLDPMEDFSLCEMGSDAL 57
Db 68 NITQDTVFTQAKPRGRILEAPPSSAAGAAQARQIESAASRDPAEYQ--DSSSGNSD 125
QY 58 ALRLACIGDEMVSUR-----APRLAQLS-EVAMHSLGLA---FIYDQT-EDIRDVLR 105
Db 126 ALELDPVSNNSDLVAQVETFTSCRPRLAQISLELANNNMDLAAAIABDPTFEEDLETLR 185
QY 106 -----SPMDGFTTLKENIMFRSPNPGSWVSCBOVLLA 139
Db 186 HMGARHSHRPHMYSTEBLEQLQTPNFLEMTTQISD-----W-SPNLVLFNEDRDLL-- 238
QY 140 LLLLALLPLLSGGL 155
Db 239 LLEVLHLNLMTEAGM 254

RESULT 15
ID 3BHS2 RAT STANDARD; PRT; 372 AA.
AC P22072;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type II
DE (3beta-HSD II) [includes: 3-beta-hydroxy-delta(5)-steroid
DE dehydrogenase (EC 1.1.1.145) (3-beta-hydroxy-5-ene steroid
DE dehydrogenase) (progesterone reductase); Steroid delta-isomerase
DE (EC 5.3.3.1) (Delta-5-3-ketosteroid isomerase)].
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91093186; PubMed=1985917;
RA Zhao H.-F., Labrie C., Simard J., de Launoit Y., Trudel C., Martel C.,
RA Rheame E., Dupont E., Luu-The V., Pelletier G., Labrie F.;
```

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RT "Characterization of rat 3 beta-hydroxysteroid dehydrogenase/delta 5-
RT delta 4 isomerase cDNAs and differential tissue-specific expression of
RT the corresponding mRNAs in steroidogenic and peripheral tissues.";
RL J. Biol. Chem. 266:583-593(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92049388; PubMed=1944305;
RA Naville D., Keeney D.S., Jenkin G., Murry B.A., Head J.R., Mason J.I.;
RT "Regulation of expression of male-specific rat liver microsomal 3
RT beta-hydroxysteroid dehydrogenase.";
RL Mol. Endocrinol. 5:1090-1100(1991).
CC -!- FUNCTION: 3beta-HSD is a bifunctional enzyme, that catalyzes the
CC oxidative conversion of delta(5)-ene-3-beta-hydroxy steroid, and
CC the oxidative conversion of ketosteroids. The 3beta-HSD enzymatic
CC system plays a crucial role in the biosynthesis of all classes of
CC hormonal steroids.
CC -!- CATALYTIC ACTIVITY: A 3-beta-hydroxy-delta(5)-steroid + NAD(+) = a
CC 3-oxo-delta(5)-steroid + NADH.
CC -!- CATALYTIC ACTIVITY: A 3-oxo-delta(5)-steroid = a 3-oxo-delta(4)-
CC steroid.
CC -!- PATHWAY: Steroid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum and mitochondrial
CC membrane-bound protein.
CC -!- TISSUE SPECIFICITY: Adrenal glands, testes and ovaries.
CC -!- SIMILARITY: Belongs to the 3beta-HSD family.
CC -!- CAUTION: Rat 3beta-HSD type II may possess only one transmembrane
CC domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; M38179; AAA63475.1; -; mRNA.
CC EMBL; S63167; AAB20228.1; -; mRNA.
DR PIR; A40378; DERTHM.
DR PIR; B39051; DERTH2.
DR Ensemble; ENSRNCG00000019454; Rattus norvegicus.
DR InterPro; IPR012272; 3beta-HSD_II.
DR InterPro; IPR002225; 3beta-HSD.
DR Pfam; PF01073; 3beta-HSD; 1.
DR PIRSF; PIRSF036679; 3beta-HSD II; 1.
KW Endoplasmic reticulum; Isomerase; Mitochondrion;
KW Multifunctional enzyme; Multigene family; NAD; Oxidoreductase;
KW Steroidogenesis; Transmembrane.
FT INIT MET 0 0 By similarity.
FT TRANS MEM 287 305 Potential.
FT NP BIND 5 36 NAD (Potential).
FT NP BIND 114 114 A -> T (in Ref. 2).
FT CONFLICT 164 164 A -> S (in Ref. 2).
FT CONFLICT 340 340 E -> V (in Ref. 2).
SQ SEQUENCE 372 AA; 42145 MW; EDAB175F3F3334B CRC64;

Query Match 10.3%; Score 83.5; DB 1; Length 372;
Best Local Similarity 24.0%; Pred.No. 22;
Matches 36; Conservative 22; Mismatches 55; Indels 37; Gaps 5;

QY 19 BOLLEPPTMEVLGNTDSEEDLPNEDFSLCEMGES--DALALRLACIG-----DEM 68
Db 26 KELQEVRLDKVFRPETKEPSKLTAKVMTLSEGDILDAQLYLRACQGISWHTASVM 85
QY 69 DVSLRAPR-----LAQLSEVAMHSLGLAFIYQOTEDIRDVLSFMDGPTTLKENI 118
Db 86 DFRSLVPRQTLIDVNLKGTQNLLEAGTHASVPAPFIYCSTDVA-----GPSYKTKTI 137
QY 119 MR-----FWESPNGSWVSCBOVLLA 139
Db 138 LNGREEEHHEHSTWSNPFPYSKMAEKAVLA 167

Search completed: March 15, 2006, 19:12:50
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Job time : 232 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2006, 19:13:04 ; Search time 47 Seconds
(without alignments)
281.449 Million cell updates/sec

Title: US-10-816-698-3
Perfect score: 809
Sequence: 1 MSEVRPLSRDILMETLLYEQ.....LILLALLPLLSGGLHLILK 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/RB COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809	100.0	160	1	US-08-408-095-27
2	809	100.0	160	2	US-09-052-877-5
3	809	100.0	160	2	US-09-709-790-5
4	472	58.3	99	2	US-09-513-999C-7729
5	284	35.1	150	2	US-09-052-877-2
6	284	35.1	150	2	US-09-709-790-2
7	177	21.9	36	1	US-08-440-391-12
8	177	21.9	36	1	US-08-908-597A-12
9	177	21.9	36	2	US-09-236-385A-12
10	177	21.9	36	4	PCT-US96-06122-12
11	142	17.6	28	1	US-08-440-391-30
12	142	17.6	28	1	US-08-908-597A-30
13	142	17.6	28	1	US-09-236-385A-30
14	142	17.6	28	4	PCT-US96-06122-30
15	138	17.1	27	2	US-09-544-664B-16
16	135	16.7	28	1	US-08-440-391-9
17	135	16.7	28	1	US-08-908-597A-9
18	135	16.7	28	2	US-09-236-385A-9
19	135	16.7	28	4	PCT-US96-06122-9
20	98	12.1	20	2	US-09-236-385A-41
21	92	11.4	15	1	US-08-632-514C-15
22	92	11.4	15	2	US-09-188-177-15
23	81.5	10.1	392	1	US-08-282-197C-60
24	80	9.9	16	2	US-09-544-664B-43
25	77	9.5	1198	2	US-09-252-991A-21016
26	75.5	9.3	414	1	US-08-845-161A-2
27	75.5	9.3	414	2	US-09-270-751-2

28	75.5	9.3	414	2	US-09-168-218B-4	Sequence 4, Appli
29	75	9.3	320	2	US-08-852-730-9	Sequence 9, Appli
30	75	9.3	340	2	US-09-722-441-10	Sequence 10, Appli
31	74	9.1	15	1	US-08-440-391-7	Sequence 7, Appli
32	74	9.1	15	1	US-08-440-391-32	Sequence 32, Appli
33	74	9.1	15	1	US-08-908-597A-7	Sequence 7, Appli
34	74	9.1	15	1	US-08-908-597A-32	Sequence 32, Appli
35	74	9.1	15	2	US-09-236-385A-7	Sequence 7, Appli
36	74	9.1	15	2	US-09-236-385A-32	Sequence 32, Appli
37	74	9.1	15	4	PCT-US96-06122-7	Sequence 7, Appli
38	74	9.1	15	4	PCT-US96-06122-32	Sequence 32, Appli
39	74	9.1	330	2	US-09-725-957-18	Sequence 18, Appli
40	74	9.1	389	2	US-08-909-828-3	Sequence 3, Appli
41	74	9.1	389	2	US-09-725-957-3	Sequence 3, Appli
42	74	9.1	389	2	US-09-725-957-14	Sequence 14, Appli
43	73.5	9.1	877	1	US-08-916-917-2	Sequence 2, Appli
44	73.5	9.1	877	1	US-08-972-631-2	Sequence 2, Appli
45	73.5	9.1	877	1	US-08-972-629-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-408-095-27
; Sequence 27, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,095
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-408-095-27

Query Match 100.0%; Score 809; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEEDLDPMEDFDLSLCMEGSDALALR	60
DB	1	MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEEDLDPMEDFDLSLCMEGSDALALR	60
QY	61	LACIGDMDVSRAPRLAQLSEVAMHSLGLAFIYDQTDIRDVLRSFMDGFTTLKENIMR	120
DB	61	LACIGDMDVSRAPRLAQLSEVAMHSLGLAFIYDQTDIRDVLRSFMDGFTTLKENIMR	120

Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 2

US-09-052-877-5
; Sequence 5, Application US/09052877
; Patent No. 6190912
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
; THEREOF IN APOPTOSIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,877
; FILING DATE: 31-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 480140.433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-052-877-5

Query Match 100.0%; Score 809; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
Qy 61 LACIGDEMVDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 3

US-09-709-790-5
; Sequence 5, Application US/09709790
; Patent No. 6600024
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
; THEREOF IN APOPTOSIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/709,790
; FILING DATE: 07-No. 6600024-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/052,877
; FILING DATE: 31-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 480140.433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-09-709-790-5

Query Match 100.0%; Score 809; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 4.9e-92;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
Qy 61 LACIGDEMVDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 4

US-09-513-999C-7729
; Sequence 7729, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duciert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7729
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE

LOCATION: 66
OTHER INFORMATION: Xaa=Leu or Met or Val
FEATURE:
NAME/KEY: UNSURE
LOCATION: 86
OTHER INFORMATION: Xaa=Ala or Asp or Gly or Val
FEATURE:
NAME/KEY: UNSURE
LOCATION: 99
OTHER INFORMATION: Xaa=Ala or Glu
US-09-513-999C-7729

Query Match 58.3%; Score 472; DB 2; Length 99;
Best Local Similarity 96.9%; Pred. No. 1.4e-50;
Matches 93; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 20 QLLPPTMEVLGMDTSEEDLPDMEDFDSLECMGSDALALRLACIGDMVSLRAPLQAQ 79
Db 3 RLLEPPTMEVLGMDTSEEDLPDMEDFDSLECMGSDALALRLACIGDMVSLRAPLQAQ 62

Qy 80 LSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLK 115
Db 63 LSEXAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLK 98

RESULT 5
US-09-052-877-2
Sequence 2, Application US/09052877
Patent No. 6190912
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
TITLE OF INVENTION: THEREOF IN APOPTOSIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,877
FILING DATE: 31-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION/DOCKET NUMBER: 480140.433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2

US-09-052-877-2

Query Match 35.1%; Score 284; DB 2; Length 150;
Best Local Similarity 42.5%; Pred. No. 5e-27;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLPDMEDFDSLECMGSDALALR 60
Db 1 MSEARLMARDVI-KTVPHQVQPP---VASETPSMK--EPVRDVLMECVGRNQVALR 54

RESULT 6
US-09-709-790-2
Sequence 2, Application US/09709790
Patent No. 6600024
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
TITLE OF INVENTION: THEREOF IN APOPTOSIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,790
FILING DATE: 07-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/052,877
FILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION/DOCKET NUMBER: 480140.433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2

US-09-709-790-2

Query Match 35.1%; Score 284; DB 2; Length 150;
Best Local Similarity 42.5%; Pred. No. 5e-27;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLPDMEDFDSLECMGSDALALR 60
Db 1 MSEARLMARDVI-KTVPHQVQPP---VASETPSMK--EPVRDVLMECVGRNQVALR 54

RESULT 7
US-08-440-391-12
Sequence 12, Application US/08440391

Qy 61 LACIGDEMVDLSRAPLQAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
Db 55 LACIGDEMVDLSRAPLQAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 111

Qy 121 FWRSPNPGSWVSCQVLLALALLLALLLPLLSGGHLHLK 160
Db 112 -WRVLTGAWVSPDQPGQLFPMVLLVLLGGAWYLQIQ 150

RESULT 6
US-09-709-790-2
Sequence 2, Application US/09709790
Patent No. 6600024
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
TITLE OF INVENTION: THEREOF IN APOPTOSIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/709,790
FILING DATE: 07-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/052,877
FILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION/DOCKET NUMBER: 480140.433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2

US-09-709-790-2

Query Match 35.1%; Score 284; DB 2; Length 150;
Best Local Similarity 42.5%; Pred. No. 5e-27;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLPDMEDFDSLECMGSDALALR 60
Db 1 MSEARLMARDVI-KTVPHQVQPP---VASETPSMK--EPVRDVLMECVGRNQVALR 54

Qy 61 LACIGDEMVDLSRAPLQAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
Db 55 LACIGDEMVDLSRAPLQAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 111

Qy 121 FWRSPNPGSWVSCQVLLALALLLALLLPLLSGGHLHLK 160
Db 112 -WRVLTGAWVSPDQPGQLFPMVLLVLLGGAWYLQIQ 150

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; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-440-391-12

Query Match 21.9%; Score 177; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 83
Db 1 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 36

RESULT 8
US-08-908-597A-12
; Sequence 12, Application US/08908597A
; Patent No. 5863795
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,597A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
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; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-908-597A-12

Query Match 21.9%; Score 177; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 83
Db 1 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 36

RESULT 9
US-09-236-385A-12
; Sequence 12, Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,385A
; FILING DATE: 25-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-236-385A-12

Query Match 21.9%; Score 177; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 83
Db 1 LECMEGSDALALRLACIGDEMVDVSLRAPRLAQLSEV 36
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RESULT 10
PCT-US96-06122-12
; Sequence 12, Application PC/TUS9606122
; GENERAL INFORMATION:
; APPLICANT: IMMUNOGEN, INC.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
; TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06122
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147PCT
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-06122-12

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Query Match 21.9%; Score 177; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 48 LECMGSDALALRLACIGDEMVSRLAPRLAQISEV 83
Db 1 LECMGSDALALRLACIGDEMVSRLAPRLAQISEV 36

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RESULT 11
US-08-440-391-30
; Sequence 30, Application US/08440391
; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-440-391-30

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Query Match 17.6%; Score 142; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 50 CMEGSDALALRLACIGDEMVSRLAPRL 77
Db 1 CMEGSDALALRLACIGDEMVSRLAPRL 28

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RESULT 12
US-08-908-597A-30
; Sequence 30, Application US/08908597A
; Patent No. 5863795
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; TITLE OF INVENTION: MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,597A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-908-597A-30

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Query Match 17.6%; Score 142; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 CMEGSDALALRLACIGDEMVDVSLRAPRL 77
Db 1 CMEGSDALALRLACIGDEMVDVSLRAPRL 28

RESULT 13
PCT-US96-385A-30
; Sequence 30, Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,385A
; FILING DATE: 25-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-236-385A-30

Query Match 17.6%; Score 142; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 CMEGSDALALRLACIGDEMVDVSLRAPRL 77
Db 1 CMEGSDALALRLACIGDEMVDVSLRAPRL 28

RESULT 14
PCT-US96-06122-30
; Sequence 30, Application PC/TUS9606122
; GENERAL INFORMATION:
; APPLICANT: IMMUNOGEN, INC.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
; WHICH MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06122
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-06122-30

Query Match 17.6%; Score 142; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 CMEGSDALALRLACIGDEMVDVSLRAPRL 77
Db 1 CMEGSDALALRLACIGDEMVDVSLRAPRL 28

RESULT 15
US-09-544-664B-16
; Sequence 16, Application US/09544664B
; Patent No. 6713280
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Wang, Jialun
; APPLICANT: Zhang, Zhiqia
; APPLICANT: Shan, Simel
; APPLICANT: Lu, Zhixian
; TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake
; FILE REFERENCE: 8321-68
; CURRENT APPLICATION NUMBER: US/09/544,664B
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/US00/09352
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,202
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 27
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily
; OTHER INFORMATION: polypeptide
US-09-544-664B-16

Query Match 17.1%; Score 138; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 CMEGSDALALRLACIGDEMVDVSLRAPR 76
Db 1 CMEGSDALALRLACIGDEMVDVSLRAPR 27

Search completed: March 15, 2006, 19:14:26
Job time : 48 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 19:13:49 ; Search time 167 Seconds
(without alignments)
400.316 Million cell updates/sec

Title: US-10-816-698-3

Perfect score: 809

Sequence: 1 MSEVRPLSRDLMTLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLCMGSGDALAUR 160

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	809	100.0	160	4	US-10-269-781-5
2	809	100.0	160	4	US-10-295-027-1373
3	809	100.0	160	4	US-10-003-632C-8
4	809	100.0	160	5	US-10-825-282-30
5	809	100.0	160	5	US-10-816-698-3
6	809	100.0	175	4	US-10-106-698-4857
7	809	100.0	175	4	US-10-264-049-2649
8	805	99.5	160	5	US-10-816-698-8
9	803	99.3	160	5	US-10-816-698-7
10	799	98.8	160	5	US-10-816-698-9
11	284	35.1	150	4	US-10-269-781-2
12	284	35.1	150	5	US-10-816-698-4
13	214	26.5	44	3	US-09-971-980-43
14	214	26.5	44	5	US-10-966-576-43
15	177	21.9	36	3	US-09-828-870-12
16	143	17.7	27	4	US-10-029-386-30479
17	142	17.6	28	3	US-09-828-870-30
18	135	16.7	28	3	US-09-828-870-9
19	135	16.7	61	3	US-09-925-299-1062
20	135	16.7	61	3	US-09-925-299-1062
21	135	16.7	61	4	US-10-106-698-6558
22	122	15.1	27	5	US-10-816-698-14
23	100	12.4	20	4	US-10-658-028A-5
24	98	12.1	20	3	US-09-828-870-41
25	87	10.8	18	5	US-10-816-698-12
26	87	10.8	18	5	US-10-816-698-13
27	85	10.5	204	4	US-10-424-599-172616

28	85	10.5	1908	4	US-10-128-714-3475	Sequence 3475, Ap
29	85	10.5	2022	4	US-10-128-714-8475	Sequence 8475, Ap
30	84.5	10.4	753	4	US-10-369-493-20200	Sequence 20200, A
31	84.5	10.4	775	5	US-10-732-923-12744	Sequence 12744, A
32	84	10.4	1120	6	US-11-097-143-31380	Sequence 31380, A
33	82.5	10.2	964	4	US-10-042-865-55	Sequence 55, Appl
34	82.5	10.2	1045	4	US-10-042-865-54	Sequence 54, Appl
35	82.5	10.2	1045	4	US-10-029-020-54	Sequence 54, Appl
36	82.5	10.2	1769	5	US-10-723-860-4494	Sequence 4494, Ap
37	82.5	10.2	2346	4	US-10-072-012-491	Sequence 491, Appl
38	82.5	10.2	2613	4	US-10-038-854-42	Sequence 42, Appl
39	82.5	10.2	2628	4	US-10-038-854-40	Sequence 40, Appl
40	82.5	10.2	2715	4	US-10-042-865-52	Sequence 52, Appl
41	82.5	10.2	2715	4	US-10-029-020-51	Sequence 51, Appl
42	82.5	10.2	2721	4	US-10-038-854-38	Sequence 38, Appl
43	82.5	10.2	2725	4	US-10-038-854-36	Sequence 36, Appl
44	79	9.8	906	4	US-10-437-963-128708	Sequence 128708, A
45	78.5	9.7	371	4	US-10-425-114-56563	Sequence 56563, A

ALIGNMENTS

RESULT 1

US-10-269-781-5
; Sequence 5, Application US/10269781
; Publication No. US20030060416A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES THEREOF IN APOPTOSIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/269,781
; FILING DATE: 11-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,877
; FILING DATE: 31-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 480140.433
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-269-781-5

Query Match 100.0%; Score 809; DB 4; Length 160;

Best Local Similarity 100.0%; Pred. No. 3.6e-79;

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MSEVRPLSRDLMTLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLCMGSGDALAUR 60
|||||

Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLECMGSDALALR 60
Qy 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 2

US-10-295-027-1373
; Sequence 1373, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1373
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1373

Query Match 100.0%; Score 809; DB 4; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.6e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLECMGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLECMGSDALALR 60
Qy 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 3

US-10-003-632C-8
; Sequence 8, Application US/10003632C
; Publication No. US20040043028A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Xianmei
; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or G
; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nucleic
; FILE REFERENCE: CEN0269
; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-8

Query Match 100.0%; Score 809; DB 4; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.6e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLECMGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSELDPMEDFDSLECMGSDALALR 60
Qy 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVDLSRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGHLHLK 160

RESULT 4

US-10-825-282-30
; Sequence 30, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-30

Query Match 100.0%; Score 809; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.6e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160
DB 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160

RESULT 5

US-10-816-698-3
; Sequence 3, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-3

Query Match 100.0%; Score 809; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.6e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160
DB 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160

RESULT 6

US-10-106-698-4857
; Sequence 4857, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0

; SEQ ID NO 4857
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4857

Query Match 100.0%; Score 809; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 4e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
DB 16 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 75
QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 76 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 135
QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160
DB 136 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 175

RESULT 7

US-10-264-049-2649
; Sequence 2649, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2649
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2649

Query Match 100.0%; Score 809; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 4e-79;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 60
DB 16 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFDSLECMGSDALALR 75
QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 76 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 135
QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 160
DB 136 FWRSPNPGSWSCQVLLALLLALLLPLLSGGLHLLK 175

RESULT 8

US-10-816-698-8
; Sequence 8, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698

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; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-8

Query Match          99.5%; Score 805; DB 5; Length 160;
Best Local Similarity 99.4%; Pred. No. 9.8e-79;
Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Qy 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160

RESULT 9
US-10-816-698-7
; Sequence 7, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-7

Query Match          99.3%; Score 803; DB 5; Length 160;
Best Local Similarity 99.4%; Pred. No. 1.6e-78;
Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Qy 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160
```

```
RESULT 10
US-10-816-698-9
; Sequence 9, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-9

Query Match          98.8%; Score 799; DB 5; Length 160;
Best Local Similarity 98.8%; Pred. No. 4.4e-78;
Matches 158; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTDEEDLDPMEDFDSLECMEGSDALALR 60
Qy 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Db 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
Qy 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160
Db 121 FWRSPNPGSWSCQVLLALLLALLLALLLPLLSGGHLHLK 160

RESULT 11
US-10-269-781-2
; Sequence 2, Application US/10269781
; Publication No. US20030060416A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: BLK GENES, GENE PRODUCTS AND USES
; THEREOF IN APOPTOSIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/269,781
; FILING DATE: 11-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,877
; FILING DATE: 31-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
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REFERENCE/DOCKET NUMBER: 480140.433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-269-781-2

Query Match 35.1%; Score 284; DB 4; Length 150;
Best Local Similarity 42.5%; Pred. No. 2.1e-22;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLPMDPDSLECMGSDALALR 60
DB 1 MSEARLMARDVI-KTVPHDQVPQP---VASETPSMK--EPVRDVLMECVGRNQVALR 54

QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 55 LACIGDEMDCILRSPLVQLPGIAIHR--LAVTYSRT-GVRGIFRSRLIRSLTNLENIWS 111

QY 121 FWRSPNPGSWVSCQEVLLALLLALLLPLLSGGHLHLK 160
DB 112 -WRVLTFGAWSPDQDQPGQLFPNVLLVFLLLGGAWYLQ 150

RESULT 12
US-10-816-698-4
; Sequence 4, Application US/10816698
; Publication No. US20050118154A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LI, YAN
; APPLICANT: WEN, YONG
; TITLE OF INVENTION: ANTI-TUMOR EFFECT OF MUTANT BIK
; FILE REFERENCE: UTSC:791US
; CURRENT APPLICATION NUMBER: US/10/816,698
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/459,901
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-816-698-4

Query Match 35.1%; Score 284; DB 5; Length 150;
Best Local Similarity 42.5%; Pred. No. 2.1e-22;
Matches 68; Conservative 33; Mismatches 49; Indels 10; Gaps 6;

QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLPMDPDSLECMGSDALALR 60
DB 1 MSEARLMARDVI-KTVPHDQVPQP---VASETPSMK--EPVRDVLMECVGRNQVALR 54

QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 55 LACIGDEMDCILRSPLVQLPGIAIHR--LAVTYSRT-GVRGIFRSRLIRSLTNLENIWS 111

QY 121 FWRSPNPGSWVSCQEVLLALLLALLLPLLSGGHLHLK 160
DB 112 -WRVLTFGAWSPDQDQPGQLFPNVLLVFLLLGGAWYLQ 150

RESULT 13

US-09-971-980-43
; Sequence 43, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1el Sequence
US-09-971-980-43

Query Match 26.5%; Score 214; DB 3; Length 44;
Best Local Similarity 95.7%; Pred. No. 1.6e-15;
Matches 44; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 96 QTEDIRDLRSFMDGFTTLKENIMRFPNPGSWVSCQVLLALL 141
DB 1 QTEDIRDLR-FMDGFTTLKENIMRFPNPGSWVSC-QVLLALL 44

RESULT 14
US-10-966-576-43
; Sequence 43, Application US/10966576
; Publication No. US20050228849A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/10/966,576
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US/09/971,980
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-10-966-576-43

Query Match 26.5%; Score 214; DB 5; Length 44;
Best Local Similarity 95.7%; Pred. No. 1.6e-15;
Matches 44; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 96 QTEDIRDLRSFMDGFTTLKENIMRFPNPGSWVSCQVLLALL 141
DB 1 QTEDIRDLR-FMDGFTTLKENIMRFPNPGSWVSC-QVLLALL 44

RESULT 15
US-09-828-870-12
; Sequence 12, Application US/09828870
; Publication No. US20040054129A1
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and

```

;
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/828,870
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/236,385
; FILING DATE: 25-JANUARY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; ATTORNEY DOCKET NO. 104322.147CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-828-870-12

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Query Match      21.9%; Score 177; DB 3; Length 36;
Best Local Similarity 100.0%; Pred.No. 1.2e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      48 LECMEGSDALALRLACIGDEMDSLRAPRLAQLSEV 83
Db      1 LECMEGSDALALRLACIGDEMDSLRAPRLAQLSEV 36

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Search completed: March 15, 2006, 19:17:18
Job time : 168 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 15, 2006, 19:14:40 ; Search time 23 Seconds
(without alignments)
199.116 Million cell updates/sec

Title: US-10-816-698-3

Perfect score: 809

Sequence: 1 MSEVRPLSRDILMETLLYEQ.....LLLLALLPLSGGHLHLK 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US12 NEW PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US13 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	12.1	20	6 US-10-981-873-8	Sequence 8, Appli
2	89	11.0	20	6 US-10-981-873-78	Sequence 78, Appl
3	87	10.8	18	6 US-10-981-873-10	Sequence 10, Appl
4	84.5	10.4	775	7 US-11-087-099-483	Sequence 483, Appl
5	82.5	10.2	1045	7 US-11-113-424-54	Sequence 54, Appl
6	82.5	10.2	1094	6 US-10-821-234-1097	Sequence 1097, Ap
7	82.5	10.2	2376	7 US-11-096-051-2	Sequence 4, Appli
8	82.5	10.2	2715	7 US-11-096-051-2	Sequence 2, Appli
9	82.5	10.2	2715	7 US-11-113-424-51	Sequence 51, Appl
10	82.5	10.2	2721	7 US-11-096-051-10	Sequence 10, Appl
11	82.5	10.2	2725	7 US-11-096-051-8	Sequence 8, Appli
12	75	9.3	286	7 US-11-055-822-44	Sequence 44, Appl
13	75	9.3	340	6 US-10-067-974-8	Sequence 8, Appli
14	75	9.3	340	7 US-11-055-822-42	Sequence 42, Appl
15	75	9.3	498	7 US-11-024-959-516	Sequence 516, Appl
16	73.5	9.1	1519	7 US-11-182-016-5	Sequence 5, Appli
17	71.5	8.8	323	6 US-10-485-517-251	Sequence 251, Appl
18	71.5	8.8	334	7 US-11-010-795-1	Sequence 1, Appli
19	71	8.8	389	7 US-11-010-795-3	Sequence 3, Appli
20	71	8.8	389	7 US-11-010-795-16	Sequence 16, Appl
21	70.5	8.7	388	7 US-11-010-795-4	Sequence 4, Appli
22	70.5	8.7	391	7 US-11-010-795-2	Sequence 2, Appli
23	70.5	8.7	1145	7 US-11-087-099-11401	Sequence 11401, A
24	70.5	8.7	1156	7 US-11-087-099-4316	Sequence 4316, Ap
25	70	8.7	14	6 US-10-981-873-49	Sequence 49, Appl

26	69	8.5	1246	6	US-10-330-773-409	Sequence 409, App
27	68.5	8.5	258	6	US-10-877-346-75	Sequence 75, Appl
28	68.5	8.5	271	6	US-10-353-783-52	Sequence 52, Appl
29	68.5	8.5	751	7	US-11-087-099-4864	Sequence 4864, Ap
30	68	8.4	1177	7	US-11-115-639-22	Sequence 22, Appl
31	68	8.4	1177	7	US-11-115-639-23	Sequence 23, Appl
32	68	8.4	1177	7	US-11-115-639-24	Sequence 24, Appl
33	68	8.4	1177	7	US-11-115-639-25	Sequence 25, Appl
34	68	8.4	1177	7	US-11-115-639-26	Sequence 26, Appl
35	68	8.4	1177	7	US-11-115-639-27	Sequence 27, Appl
36	68	8.4	1177	7	US-11-115-639-28	Sequence 28, Appl
37	68	8.4	1177	7	US-11-115-639-29	Sequence 29, Appl
38	68	8.4	1177	7	US-11-115-639-30	Sequence 30, Appl
39	68	8.4	1242	6	US-10-330-773-412	Sequence 412, App
40	67.5	8.3	1131	7	US-11-087-099-3711	Sequence 3711, Ap
41	67	8.3	1193	7	US-11-115-639-20	Sequence 19, Appl
42	67	8.3	1193	7	US-11-115-639-21	Sequence 20, Appl
43	67	8.3	1193	7	US-11-115-639-21	Sequence 21, Appl
44	66.5	8.2	218	6	US-10-714-887-158	Sequence 158, App
45	66.5	8.2	397	7	US-11-087-099-12425	Sequence 12425, A

ALIGNMENTS

RESULT 1
US-10-981-873-8
; Sequence 8, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-8

Query Match 12.1%; Score 98; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GSDALALRLACIGDEMVSLL 72

Db 1 GSDALALRLACIGDEMVSLL 20

RESULT 2

US-10-981-873-78
; Sequence 78, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873

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; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-78

Query Match 11.0%; Score 89; DB 6; Length 20;
Best Local Similarity 90.9%; Pred. No. 0.0023;
Matches 20; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 51 MEGSDALRLACIGDEMDSLSR 72
Db 1 MEGSD--ALRLACIGDEMDSLSR 20

RESULT 3
US-10-981-873-10
; Sequence 10, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; FILE OF INVENTION: US530-124001
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Naturally occurring peptide
US-10-981-873-10

Query Match 10.8%; Score 87; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 ALALRLACIGDEMDSLSR 73
Db 1 ALALRLACIGDEMDSLSR 18

RESULT 4
US-11-087-099-483
; Sequence 483, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 483
; LENGTH: 775

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; TYPE: PRT
; ORGANISM: Nostoc punctiforme
US-11-087-099-483

Query Match 10.4%; Score 84.5; DB 7; Length 775;
Best Local Similarity 26.2%; Pred. No. 0.83;
Matches 27; Conservative 25; Mismatches 36; Indels 15; Gaps 4;

Qy 37 EDLDPMEDFSLCEMGSDALALRLACIGDEMDSLSRAPRLAQISEVAMHSLGLAFIYDQ 96
Db 555 EDYAQVLDDDGIECLQTVVLSVR-----METLINA--LLRLSQ-----LGAHLREQ 600

Qy 97 TEDIRDVLSRFMDGFTTLKENI-MRFWRSPNPGSWVSCQVLL 138
Db 601 ATDLNELLNQVIDVFRASRQDSGLVDIRIPPLPTIQCDRLV 643

RESULT 5
US-11-113-424-54
; Sequence 54, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-54

Query Match 10.2%; Score 82.5; DB 7; Length 1045;
Best Local Similarity 24.3%; Pred. No. 2;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

Qy 13 METL-----LYEQLEPPPTMEVLGTDSEEDLDPMEDFSLCEMGSDALALRLACIGDEM 68
Db 248 MQTIRSIGYRNINYPPEASIIITDNE-----EGLLIQTAFLGTSR 290

Qy 69 DVSLRAPRLAQISEVAMHSLGLAFIYDQTEDIRDVLSRFMDGF 111
Db 291 RVLFKRRQRLSEILYDSTRVSYETAGVLKTVNLQSDGF 333

RESULT 6
US-10-821-234-1097
; Sequence 1097, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit

```



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; APPLICANT: Andarmani, Susan
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1097
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1097

Query Match      10.2%; Score 82.5; DB 6; Length 1094;
Best Local Similarity 24.3%; Pred. No. 2.1;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

QY 13 METL-----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
DB 297 MQTIRSIGYRNIYNPPESNAsIITDYNE-----EGLLQTAFLGTGR 339

QY 69 DVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSEFMDGF 111
DB 340 RVLFKYRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGF 382

RESULT 7
US-11-096-051-4
; Sequence 4, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE-REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; LENGTH: 2376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-4

Query Match      10.2%; Score 82.5; DB 7; Length 2376;
Best Local Similarity 24.3%; Pred. No. 5.8;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

QY 13 METL-----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
DB 1579 MQTIRSIGYRNIYNPPESNAsIITDYNE-----EGLLQTAFLGTGR 1621

QY 69 DVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSEFMDGF 111
DB 1622 RVLFKYRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGF 1664

RESULT 8
US-11-096-051-2
; Sequence 2, Application US/11096051
```

```
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-2

Query Match      10.2%; Score 82.5; DB 7; Length 2715;
Best Local Similarity 24.3%; Pred. No. 6.9;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

QY 13 METL-----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
DB 1918 MQTIRSIGYRNIYNPPESNAsIITDYNE-----EGLLQTAFLGTGR 1960

QY 69 DVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSEFMDGF 111
DB 1961 RVLFKYRQTRLSEILYDSTRVSFTYDETAGVLKTVNLQSDGF 2003

RESULT 9
US-11-113-424-51
; Sequence 51, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-113-424-51
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Query Match      10.2%; Score 82.5; DB 7; Length 2715;
Best Local Similarity 24.3%; Pred. No. 6.9;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

Qy 13 METL----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
Db 1918 MQTIRSIGYRNINYPNESNASIITDNE-----EGLLLQTAFLGTSR 1960

Qy 69 DVSLRAPRLAQLSEVAMHSLGLAFIYDQTEIRDLVLSRFMDGF 111
Db 1961 RVLFKYRQRLSELILYDSTRVSFTYDTAGVLKTVNLQSDGF 2003

RESULT 10
US-11-096-051-10
; Sequence 10, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: 60/557,978
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 10
; LENGTH: 2721
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-10

Query Match      10.2%; Score 82.5; DB 7; Length 2721;
Best Local Similarity 24.3%; Pred. No. 6.9;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

Qy 13 METL----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
Db 1924 MQTIRSIGYRNINYPNESNASIITDNE-----EGLLLQTAFLGTSR 1966

Qy 69 DVSLRAPRLAQLSEVAMHSLGLAFIYDQTEIRDLVLSRFMDGF 111
Db 1967 RVLFKYRQRLSELILYDSTRVSFTYDTAGVLKTVNLQSDGF 2009

RESULT 11
US-11-096-051-8
; Sequence 8, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
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; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 8
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-8

Query Match      10.2%; Score 82.5; DB 7; Length 2725;
Best Local Similarity 24.3%; Pred. No. 6.9;
Matches 25; Conservative 15; Mismatches 42; Indels 21; Gaps 2;

Qy 13 METL----LYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALRLACIGDEM 68
Db 1928 MQTIRSIGYRNINYPNESNASIITDNE-----EGLLLQTAFLGTSR 1970

Qy 69 DVSLRAPRLAQLSEVAMHSLGLAFIYDQTEIRDLVLSRFMDGF 111
Db 1971 RVLFKYRQRLSELILYDSTRVSFTYDTAGVLKTVNLQSDGF 2013

RESULT 12
US-11-055-822-44
; Sequence 44, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 44
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-44

Query Match      9.3%; Score 75; DB 7; Length 286;
Best Local Similarity 24.1%; Pred. No. 2.3;
Matches 32; Conservative 25; Mismatches 58; Indels 18; Gaps 5;

Qy 13 METLLYEQLLEPPPTMEVLGMDTSEEDLDPMBD-FDSLECMGSDALALRLACIGDEM 71
Db 38 VEKLIHQ----PDMDLVGIFSRRLDTKTPTFVDVADVDKHDVDVFLFLCMGSDATDIP 93
```

QY 72 LRAPLAQLSEVAMHSLGLAFIYDQTEDIRDV--LRSPMDGFTTLKENIMRFRSPNPGS 129
 Db 94 EQAPKFAQ-----FACTVDYDNRDIPRHRQVMEAEATAAGNVALVSTGWDPCGM 143

QY 130 WVSCEQVLLALL 142
 Db 144 F-SINRVYAAAVL 155

RESULT 13

US-10-067-974-8
 ; Sequence 8, Application US/10067974
 ; Publication No. US2005025037A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Lihing-Yew
 ; APPLICANT: Trei, Kelli J.
 ; TITLE OF INVENTION: Polynucleotide Constructs for Increased Lysine Production
 ; FILE REFERENCE: 1533.2640001
 ; CURRENT APPLICATION NUMBER: US/10/067,974
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: 60/267,183
 ; PRIOR FILING DATE: 2001-02-08
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-10-067-974-8

Query Match 9.3%; Score 75; DB 6; Length 340;
 Best Local Similarity 24.1%; Pred. No. 2.8; Indels 18; Gaps 5;
 Matches 32; Conservative 25; Mismatches 58

QY 13 METLLYEQLLEPPTMEVLGMDTSEEDLPMD--FDSLECMGSDALALRLACIGDEMVDVS 71
 Db 38 VEKLIKQ-----PMDLVGIFSRATLDTKTPFVDVADVDKHAADDVDFVFLCMGSAATDIP 93

QY 72 LRAPLAQLSEVAMHSLGLAFIYDQTEDIRDV--LRSPMDGFTTLKENIMRFRSPNPGS 129
 Db 94 EQAPKFAQ-----FACTVDYDNRDIPRHRQVMEAEATAAGNVALVSTGWDPCGM 143

QY 130 WVSCEQVLLALL 142
 Db 144 F-SINRVYAAAVL 155

RESULT 14

US-11-055-822-42
 ; Sequence 42, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompeius, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 42
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-055-822-42

Query Match 9.3%; Score 75; DB 7; Length 340;
 Best Local Similarity 24.1%; Pred. No. 2.8; Indels 18; Gaps 5;
 Matches 32; Conservative 25; Mismatches 58

QY 13 METLLYEQLLEPPTMEVLGMDTSEEDLPMD--FDSLECMGSDALALRLACIGDEMVDVS 71
 Db 38 VEKLIKQ-----PMDLVGIFSRATLDTKTPFVDVADVDKHAADDVDFVFLCMGSAATDIP 93

QY 72 LRAPLAQLSEVAMHSLGLAFIYDQTEDIRDV--LRSPMDGFTTLKENIMRFRSPNPGS 129
 Db 94 EQAPKFAQ-----FACTVDYDNRDIPRHRQVMEAEATAAGNVALVSTGWDPCGM 143

QY 130 WVSCEQVLLALL 142
 Db 144 F-SINRVYAAAVL 155

RESULT 15

US-11-024-959-516
 ; Sequence 516, Application US/11024959
 ; Publication No. US20060010516A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSTER, RICHARD L.
 ; APPLICANT: CONNETT, MARIE B.
 ; APPLICANT: EMERSON, SARAH JANE
 ; APPLICANT: GRIGOR, MURRAY ROBERT
 ; APPLICANT: HIGGINS, COLLEEN M.
 ; APPLICANT: LUND, STEVEN TROY
 ; APPLICANT: MAGUSIN, ANDREAS
 ; APPLICANT: KODRZYCKI, BOB
 ; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
 ; FILE REFERENCE: 04463-0360
 ; CURRENT APPLICATION NUMBER: US/11/024,959
 ; CURRENT FILING DATE: 2004-12-30
 ; PRIOR APPLICATION NUMBER: 60/533,036
 ; PRIOR FILING DATE: 2003-12-30
 ; NUMBER OF SEQ ID NOS: 782
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 516
 ; LENGTH: 498
 ; TYPE: PRT
 ; ORGANISM: Eucalyptus sp.
 US-11-024-959-516

Query Match 9.3%; Score 75; DB 7; Length 498;
 Best Local Similarity 28.2%; Pred. No. 4.6; Indels 24; Gaps 6;
 Matches 31; Conservative 18; Mismatches 37

QY 20 QLLEPPTMEVL-----GMTDSEEDLPMD--FDSLECMGSDALALRLACIGDEMVDVS 72
 Db 18 EVAEPPSKEEIEILKSGVVERSGSDGEEEDNM-----DAVASEKA---DEVSTALS 68

QY 73 RAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSP--MDGFTTLKENIMRFRSPNPGS 121
 Db 69 AADALGRISKVKAGSGF-----EDIADGLRELDMDNYDEDEEDVKLIF 111

Search completed: March 15, 2006, 19:17:47
Job time : 24 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: March 15, 2006, 19:05:25 ; Search time 188 Seconds
(without alignment)
373.939 Million cell updates/sec

Title: US-10-816-698-3
Perfect score: 809
Sequence: 1 MSEVPLSRDLMTLLYEQ.....LLLLALLPLLSGGLHLLK 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809	100.0	160	2	AAW01000 Apoptosis
2	809	100.0	160	2	AAW94326 Human Bip
3	809	100.0	160	2	AAY05436 Human BIK
4	809	100.0	160	7	ADN40055 Cancer/an
5	809	100.0	160	8	ADJ66632 Bcl-2 int
6	809	100.0	160	8	ADL69728 Human Bcl
7	809	100.0	160	8	ADT77553 Wild type
8	809	100.0	160	8	ADU22889 Human apo
9	809	100.0	160	9	ADZ09814 Human bre
10	809	100.0	175	4	AAG74083 Human col
11	809	100.0	175	5	ABP41517 Human ova
12	809	100.0	378	6	AAG37657 Bcl2 rela
13	805	99.5	160	8	ADT77558 Ser35Asp
14	803	99.3	160	8	ADT77557 Thr33Asp
15	799	98.8	160	8	ADT77559 Thr33Asp
16	472	58.3	99	3	AAG03648 Human sec
17	284	35.1	150	2	AAY42853 Murine pr
18	284	35.1	150	8	ADT77554 BIK polyd
19	177	21.9	36	5	AAU77887 Bip1a pep
20	177	21.9	36	8	ADK14699 Bak GD do
21	143	17.7	27	8	ABO56845 Human gen
22	142	17.6	28	2	AAW06301 GD domain
23	142	17.6	28	5	AAU77897 Bip1a GD
24	142	17.6	28	8	ADK14717 Bcl-2 rel

25	138	17.1	27	3	AAB37016	Aab37016 Bcl2 poly
26	135	16.7	28	5	AAU77884	Aau77884 Bip1a GD
27	135	16.7	28	8	ADK14696	Adk14696 Bcl-2 rel
28	135	16.7	61	3	AAB53522	Aab53522 Human col
29	135	16.7	61	4	AAG75784	Aag75784 Human col
30	127	15.7	26	3	RAY96324	Ray96324 Mammalian
31	127	15.7	26	4	AAB70374	Aab70374 BIK BH3 c
32	124	15.3	25	9	ABE79162	Abe79162 BH3 pepci
33	122	15.1	27	8	ADT77564	Adt77564 Bik trans
34	108	13.3	22	9	AEA04889	Aea04889 BCL-2 pro
35	100	12.4	20	8	ADK90777	Adk90777 BIKBH3 pe
36	98	12.1	20	5	AAU77896	Aau77896 Bip1a pep
37	98	12.1	20	8	ADK14728	Adk14728 Bcl-2 rel
38	98	12.1	20	9	AEA04818	Aea04818 BCL-2 pro
39	87	10.8	18	8	ADT77563	Adt77563 Bik heter
40	87	10.8	18	8	ADT77562	Adt77562 Bik Bcl-2
41	87	10.8	18	9	AEA04820	Aea04820 BCL-2 pro
42	85	10.5	1908	6	ABJ25817	Abj25817 Aspergill
43	85	10.5	2022	6	ABJ26417	Abj26417 Aspergill
44	84.5	10.4	753	8	ADS41770	Ads41770 Bacterial
45	84	10.4	1120	4	ABB68196	Abb68196 Drosophil

ALIGNMENTS

RESULT 1
AAW01000
ID AAW01000 standard; protein; 160 AA.
XX
AC AAW01000;
XX
DT 18-DEC-1996 (first entry)
XX
DE Apoptosis-regulating protein Bip1A.
XX
KW Apoptosis-regulating protein; Bip1A; adenovirus E1B 19K protein; Bcl-2;
KW oncogene; cell death; cancer; tumour; immune disorder; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN EP733706-A2.
XX
PD 25-SEP-1996.
XX
PF 21-MAR-1996; 96EP-00104542.
XX
PR 21-MAR-1995; 95US-00408095.
XX
XX (UYSL-) UNIV ST LOUIS.
XX
XX Chinnadurai G;
XX
XX WPI; 1996-427055/43.
XX
XX N-PSDB; AAT38230.
XX
XX Nucleic acids encoding apoptosis regulating proteins - useful for
diagnosing and treating immune disorders, malignancies, etc.
XX
XX Claim 1; Page 47; 60pp; English.
XX
XX Apoptosis-regulating protein Bip1A (AAW01000) specifically interacts with
motifs (see also AAW01003-06) on apoptosis-blocking proteins E1B 19K
(AAW01010) and Bcl-2 (AAW01018). Its amino acid sequence was deduced from
a cDNA clone (AAT38230) isolated from a human cDNA library using a yeast
two-hybrid assay with Bcl-2 as bait. Apoptosis-regulating proteins (see
also AAW00997-99 and AAW00101-W01002) can be used diagnostically or to
regulate cell death, e.g. to counteract high levels of Bcl-2 associated
with certain malignancies
XX
XX Sequence 160 AA;

Query Match 100.0%; Score 809; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 Db 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

Qy 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120
 Db 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120

Qy 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160
 Db 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160

RESULT 2
 AAW94326
 ID AAW94326 standard; protein; 160 AA.
 XX
 AC AAW94326;
 XX
 DT 13-APR-1999 (first entry)
 XX
 DE Human BiplA protein.
 XX
 KW Human; Nip1; Nip2; Nip3; BiplA; Bips; Bip13; adenovirus; cell death;
 KW viral infection; Bcl-2; protooncogene; mutational analysis; apoptosis;
 KW E1B 19K protein; cell survival regulation.
 XX
 OS Homo sapiens.
 XX
 FN US5858678-A.
 XX
 PD 12-JAN-1999.
 XX
 PF 21-MAR-1995; 95US-00408095.
 XX
 PR 02-AUG-1994; 94US-00284139.
 XX
 PA (UYSL-) UNIV ST LOUIS.
 XX
 PI Chinnadurai G;
 XX
 DR WPI; 1999-152099/13.
 DR N-PSDB; AAX04122.
 XX
 PT Polypeptides that bind to anti-apoptotic proteins - useful for protecting
 PT against cell death induced by viral infection and to modulate response to
 PT physical and chemical stimuli.
 XX
 PS Claim 1; Col 61-62; 41pp; English.
 XX
 CC The present invention describes: (1) a method for regulating cell death,
 CC comprising exposing an isolated cell to a polypeptide selected from Nip1,
 CC Nip2, Nip3, BiplA, Bips and Bip13; (2) a method for neutralising the
 CC activity of the adenovirus E1B 19 kD protein, the Bcl-2 protein or the
 CC BHRF-1 protein, comprising exposing an isolated cell to a polypeptide as
 CC in (1); and (3) a method for detecting molecules that bind to at least
 CC one polypeptide as in (1), comprising lysing cells, exposing the lysate
 CC to the polypeptide and detecting any molecule- polypeptide aggregates.
 CC The methods are useful for providing proteins able to bind to other
 CC proteins known to regulate cell survival e.g. it is known that E1B 19K
 CC protein provides a survival function similar to the cellular
 CC protooncogene bcl-2 gene product which is able to block apoptosis in
 CC haematopoietic B and T cells. The present sequence represents human
 CC BiplA, given in the present invention
 XX
 SQ Sequence 160 AA;

Query Match 100.0%; Score 809; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 Db 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

Qy 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120
 Db 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120

Qy 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160
 Db 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160

Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 Db 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

Qy 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120
 Db 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120

Qy 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160
 Db 121 FWRSPNGSNWSCQVLLALLLALLLPLLSGGLHLLK 160

RESULT 3
 AAY05436
 ID AAY05436 standard; peptide; 160 AA.
 XX
 AC AAY05436;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BIK protein sequence.
 XX
 KW BH3 domain; cell death agonist; bcl homology domain; Bcl-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW autoantibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO9916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 22-SEP-1998; 98WO-US019765.
 XX
 PR 26-SEP-1997; 97US-0060133P.
 PR 07-OCT-1997; 97US-00946039.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 1999-255058/21.
 XX
 PT Bcl homology domain 3 polypeptide.
 XX
 PS Disclosure; Fig 21e; 104pp; English.
 XX
 CC This sequence represents the human BIK protein. The invention relates to
 CC a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member
 CC of the Bcl-2 family. The BH3 polypeptide can be used in a method for
 CC promoting apoptosis in a target cell, especially where the cell is a
 CC cancer cell a virus infected cell or an autoantibody producing cell. The
 CC BH3 polypeptide can be used in therapeutic compositions for treating
 CC disease including cancer, other lymphoproliferative conditions,
 CC arthritis, inflammation, and autoimmune diseases, which may result from
 CC the down regulation of cell death regulation
 XX
 SQ Sequence 160 AA;

Query Match 100.0%; Score 809; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 Db 1 MSEVRPLSRDILMETLLYEQLLEPTTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60

Qy 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120
 Db 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSPMDGFTTLKENIMR 120

Db 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120

Qy 121 FWRSPNPGSVSWCEQVLLALLLALLLPLLSGGLHLHLK 160

Db 121 FWRSPNPGSVSWCEQVLLALLLALLLPLLSGGLHLHLK 160

RESULT 4

ADN40055

ID ADN40055 standard; protein; 160 AA.

XX AC ADN40055;

XX DT 17-JUN-2004 (first entry)

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C425.

XX KW Human; differential expression; cancer; angiogenic disorder;

XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

XX KW inflammatory disease; autoimmune disease;

XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;

XX KW detection; diagnosis; prognosis; drug screening; drug targeting;

XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

XX KW vulnery; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2002; 2002WO-US036810.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 21-NOV-2001; 2001US-0332464P.

XX PR 29-NOV-2001; 2001US-0334393P.

XX PR 03-DEC-2001; 2001US-0335394P.

XX PR 14-DEC-2001; 2001US-0340376P.

XX PR 08-JAN-2002; 2002US-0347211P.

XX PR 10-JAN-2002; 2002US-0347349P.

XX PR 08-FEB-2002; 2002US-0355250P.

XX PR 13-FEB-2002; 2002US-0356714P.

XX PR 20-FEB-2002; 2002US-0359077P.

XX PR 29-MAR-2002; 2002US-0368809P.

XX PR 04-APR-2002; 2002US-0370110P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PR 05-JUN-2002; 2002US-0386614P.

XX PR 16-JUL-2002; 2002US-0396839P.

XX PR 22-JUL-2002; 2002US-0397775P.

XX PR 22-JUL-2002; 2002US-0397845P.

XX PR 09-SEP-2002; 2002US-0409450P.

XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX AFar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI; 2003-468649/44.

XX N-PSDB; ADN39838.

XX Determining the presence or absence of a pathological cell in a patient.

XX useful for diagnosing, prognosing or treating cancer, comprises detecting

XX a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C425; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

XX whose expression is upregulated or downregulated in specific cancers or

XX other diseases such as angiogenic or fibrotic disorders, and to methods

XX of determining the presence or absence of a pathological cell in a

XX patient by detecting a nucleic acid at least 80% identical to those of

XX the invention or by detecting a polypeptide of the invention. The

XX invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a

CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the

CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present

CC sequence represents a polypeptide of the invention.

XX Sequence 160 AA;

Qy 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPNEDFSLCEMGSDALALR 60

Db 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPNEDFSLCEMGSDALALR 60

Qy 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120

Db 61 LACIGDEMVSRLAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120

Qy 121 FWRSPNPGSVSWCEQVLLALLLALLLPLLSGGLHLHLK 160

Db 121 FWRSPNPGSVSWCEQVLLALLLALLLPLLSGGLHLHLK 160

RESULT 5

ADJ66632

ID ADJ66632 standard; protein; 160 AA.

XX AC ADJ66632;

XX DT 06-MAY-2004 (first entry)

XX DE Bcl-2 interacting killer (Bik) protein for anti-cancer protein complex.

XX KW neuroprotective; cytostatic; gene therapy; protein complex;

XX KW cellular network; cancer; neurodegenerative disease; drug target.

XX OS Homo sapiens.

XX PN WO2004009622-A2.

XX PD 29-JAN-2004.

XX PF 18-JUL-2003; 2003WO-EP007835.

XX PR 19-JUL-2002; 2002EP-00016109.

XX PR 19-JUL-2002; 2002EP-00016111.

XX PR 19-JUL-2002; 2002EP-00016123.

XX PR 19-JUL-2002; 2002EP-00016128.

XX PR 22-JUL-2002; 2002EP-00016427.

XX (CELL-) CELLZONE AG.

XX Merino A, Bouwmeester T, Bauer A, Drewes G, Marzioch M, Kruse U;

XX Superti-Furga G, Eberhard D, Ruffner H, Hobson S, Helftenbein G;

XX Cruciat C;

XX WPI; 2004-123372/12.

XX New protein complexes of cellular networks underlying the development of

XX cancer and other diseases, useful for diagnosing and/or treating

XX neurodegenerative diseases or cancer, and in drug screening.

XX Disclosure; SEQ ID NO 162; 809pp; English.

XX The invention relates to a protein complex of cellular networks

XX underlying the development of cancer and other diseases. The complex (I)

CC comprises at least one first and second proteins selected from any of the
 CC proteins listed in the specification, or their functionally active
 CC derivatives, fragments, homologues or variants, the variants being
 CC encoded by a nucleic acid that hybridizes to the nucleic acid encoding
 CC the protein under low stringency conditions. A complex (II) comprises at
 CC least two of the second proteins, where the low stringency conditions
 CC comprise hybridization in a buffer comprising 35% formamide, 5 x SSC, 50
 CC mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 microg/ml
 CC denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20
 CC hours at 40 deg C, washing in a buffer consisting of 2 x SSC, 25 mM Tris-
 CC HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 deg C, and
 CC EDTA, and 0.1% SDS for 1.5 hours at 60 deg C. The composition and methods
 CC are useful in diagnosing or treating diseases and disorders, preferably
 CC neurodegenerative diseases. These may also be used as a drug target or in
 CC manufacturing a medicament for the treatment or prevention of the above-
 CC mentioned diseases or disorders. The composition may also be used for
 CC treating cancer. This sequence represents one of the proteins of the
 CC complex of the invention.

XX SQ Sequence 160 AA;

Query Match 100.0%; Score 809; DB 8; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
 DB 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
 QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGGLHLK 160
 DB 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGGLHLK 160

RESULT 6

ADL69728
 ID ADL69728 standard; protein; 160 AA.
 AC ADL69728;
 XX
 DT 20-MAY-2004 (first entry)
 DE Human Bcl2 related protein #8.
 XX
 KW Bcl2 related protein; therapeutic protein; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004043028-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 02-NOV-2001; 2001US-00003632.
 XX
 PR 02-NOV-2001; 2001US-00003632.
 XX
 PA (LEEC/) LEE C.
 PA (SHIX/) SHI X.
 PA (LYCC/) LY C.
 PA (MOOR/) MOORE G.
 XX
 PI Lee C, Shi X, Ly C, Moore G;
 XX
 DR WPI; 2004-225672/21.
 XX
 PT New Bcl2 encoding nucleic acids for enhancing growth and/or production of
 PT therapeutic or diagnostic proteins from cultured mammalian host cells.

PS Disclosure; SEQ ID NO 8; 42pp; English.
 XX
 CC The invention relates to a protein expression enhancing Bcl2 related
 CC nucleic acid comprising a first nucleic acid encoding at least one
 CC expressible protein and a second nucleic acid encoding at least one Bcl2
 CC related protein, where expression of the expressible protein is enhanced
 CC by transcription or translation of the second nucleic acid. The
 CC composition and methods are useful for enhancing growth and/or production
 CC of therapeutic or diagnostic proteins from cultured mammalian host cells.
 CC The present sequence is human Bcl2 related protein.

XX SQ Sequence 160 AA;

Query Match 100.0%; Score 809; DB 8; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
 DB 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
 QY 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGGLHLK 160
 DB 121 FWRSPNPGSWSCQVLLALLLALLLPLLSGGGLHLK 160

RESULT 7

ADT77553
 ID ADT77553 standard; protein; 160 AA.
 XX
 AC ADT77553;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Wild type Bik.
 XX
 KW Bik; nbk; pro-apoptotic; BH3-only protein; Bcl-2 homology region;
 KW BH3 domain; initiator; apoptosis; chromosome 22q; human; breast; colon;
 KW cancer; cell proliferation; phosphorylation; protein transduction domain;
 KW inhibition; proliferative disorder; hematologic malignancy; sarcoma;
 KW leukaemia; lymphoma; myeloma; prostate; ovarian; lung; brain; pancreatic;
 KW liver; bladder; gastrointestinal cancer; oestrogen receptor positive;
 KW EGF receptor overexpressing; optionally overexpressing Her2/neu-;
 KW Akt overexpressing; androgen dependent; restenosis; sensitizing; tumour;
 KW chemotherapeutic agent; antitumour activity.
 XX
 OS Homo sapiens.
 XX
 PN WO2004089981-A2.
 XX
 PD 21-OCT-2004.
 XX
 PF 02-APR-2004; 2004WO-US010342.
 XX
 PR 02-APR-2003; 2003US-0459901P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Hung M, Li Y, Wen Y;
 XX
 DR WPI; 2004-748724/73.
 DR N-PSDB; ADT77555, ADT77556.
 DR GENBANK; AAC50413, NP_001188, AAF01156, AAC79124, CAA62013, S58214.
 XX
 PT New mutant Bik polypeptides having anti-cell proliferation activity
 PT and/or pro-apoptotic activity useful for the treatment of cancer.
 XX
 PS Disclosure; SEQ ID NO 3; 152pp; English.
 XX

This sequence is encoded by the genomic DNA sequence encoding wild type BIK. BIK, also known as nbk, is one of the pro-apoptotic BH3-only proteins, which have only one of the Bcl-2 homology regions BH3 domains, and have recently been recognised as essential initiators of apoptosis. BIK is located on chromosome 22q. Loss of informative alleles in this region may be related to the development of human breast and colon cancer. The mutant BIK polypeptides of the invention have anti-cell proliferation activity and/or pro-apoptotic activity. Wild type BIK is mutated at either Thr33, Ser35 or both Thr33 and Ser35. These substitutions prevent the phosphorylation of mutant BIK under conditions that would result in phosphorylation of an unsubstituted BIK polypeptide. The mutant BIK polypeptide further comprises a protein transduction domain and is complexed with a lipid. The mutant BIK of the invention is used for inhibiting cell proliferation in the treatment of a proliferative disorder e.g. cancer (such as hematologic malignancies, sarcoma, leukaemia, lymphoma, myeloma, breast, prostate, ovarian, lung, brain, pancreatic, liver, bladder or gastrointestinal cancer (including oestrogen receptor positive, EGF receptor overexpressing, optionally overexpressing Her2/neu-, Akt overexpressing and optionally androgen dependent cancers)) and restenosis in an animal (such as human); and for sensitizing the tumour cell to a chemotherapeutic agent. The mutant BIK polypeptides exhibit anti-cell proliferation activity and/or pro-apoptotic activity i.e. substantially the same or more effective than the native BIK polypeptides and are capable of exhibiting strong antitumour activity in both in vivo and in vitro cells. The polypeptides sensitize the tumour cell to the chemotherapeutic agent and enhance the chemotherapeutic agent-induced apoptosis of the cells, thus are useful for the treatment of resistant tumours.

Query Match 100.0%; Score 809; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 8.4e-88;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLHLK 160

RESULT 8
ADU22889
ID ADU22889 standard; protein; 160 AA.
XX AC ADU22889;
XX DT 27-JAN-2005 (first entry)
XX DE Human apoptosis inducing BIK protein.
XX KW apoptosis modulation; cytostatic; antiinflammatory; neuroprotective;
XX KW muscular-gen.; antiarthritic; antirheumatic; antidiabetic;
XX KW immunosuppressive; cancer; T-lymphocyte; rheumatoid arthritis;
XX KW insulin dependent diabetes; multiple sclerosis;
XX KW systemic lupus erythematosus; myasthenia gravis;
XX KW graft versus host disease; BIK.
XX OS Homo sapiens.
XX FN US2004224389-A1.
XX PD 11-NOV-2004.
XX PF 14-APR-2004; 2004US-00825282.

27-MAY-1994; 94US-00250478.
26-JAN-1995; 95US-00378507.
29-MAY-1998; 98US-00087195.
17-MAY-1999; 99US-0134416P.
08-DEC-1999; 99US-00456357.
XX (COLS) UNIV COLORADO.
XX Bellgrau D, Duke RC, Schaack JB;
XX WPI; 2004-794697/78.
XX N-85DB; ADU22888.
PT Propagating a recombinant viral vector comprising a nucleic acid sequence
PT encoding an apoptosis-inducing protein by culturing a cell transfected
PT with a recombinant nucleic acid sequence encoding an apoptosis-inhibiting
PT protein.
PS Claim 12; SEQ ID NO 30; 106pp; English.
CC The invention relates to a novel method for propagating a recombinant
CC viral vector comprising a nucleic acid sequence encoding an apoptosis-
CC inducing protein. The method comprises culturing an isolated cell
CC transfected with a recombinant nucleic acid molecule encoding a protein
CC that inhibits apoptosis, operatively linked to a transcription control
CC sequence, and a recombinant viral vector comprising a nucleic acid
CC sequence encoding a protein that induces apoptosis, operatively linked to
CC a transcription control sequence. The method of the invention
CC demonstrates cytostatic, antiinflammatory, neuroprotective, muscular-
CC gen., antiarthritic, antirheumatic, antidiabetic and immunosuppressive
CC applications. The method may be useful for inducing apoptosis in cancer
CC cells or for suppressing a T-lymphocyte-mediated disease, such as,
CC rheumatoid arthritis, insulin dependent diabetes, multiple sclerosis,
CC systemic lupus erythematosus, myasthenia gravis or graft versus host
CC disease. The current sequence is that of the human apoptosis inducing BIK
CC protein of the invention.
XX Sequence 160 AA;
Query Match 100.0%; Score 809; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 8.4e-88;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLEPPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSVLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDLVRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLHLK 160
RESULT 9
ADZ09814
ID ADZ09814 standard; protein; 160 AA.
XX AC ADZ09814;
XX DT 30-JUN-2005 (first entry)
XX DE Human breast cancer marker BIK protein.
XX KW neoplasm; tumor marker; cytostatic; breast tumor; gene therapy; BIK.
XX KW Homo sapiens.
XX OS EP1522594-A2.
XX FN 13-APR-2005.

XX PF 30-JUN-2004; 2004EP-00015374.
 XX PR 06-OCT-2003; 2003EP-00022587.
 XX PA (FARB) BAYER HEALTHCARE AG.
 XX PI Munnes M, Bojar H;
 XX WPI; 2005-265481/28.
 DR N-PSDB; AD209649.
 XX
 PT Characterizing the state of a neoplastic disease in a subject by
 PT comparing the pattern of determined expression levels of marker genes in
 PT a biological sample with reference patterns of expression levels.
 XX
 PS Disclosure; SEQ ID NO 258; 542pp; English.
 XX
 CC The invention relates to a novel method for characterizing the state of a
 CC neoplastic disease in a subject comprising determining the pattern of
 CC expression levels of at least 6, 8,10,15, 20, 30, 47 or 67 marker genes
 CC in a biological sample, comparing the pattern of expression levels with
 CC reference patterns of expression levels and characterizing the state of
 CC the neoplastic disease in the subject from the outcome of the comparison.
 CC The method of the invention demonstrates cytostatic applications and may
 CC be useful in characterizing the state of a neoplastic disease in a
 CC subject, preferably breast cancer, in gene therapy and for screening for
 CC compounds having a curative effect on a neoplastic disease. The current
 CC sequence is that of the human breast cancer marker BIK protein of the
 CC invention which is differentially expressed in neoplastic tissue.
 XX
 SQ Sequence 160 AA;

Query Match 100.0%; Score 809; DB 9; Length 160;
 Best Local Similarity 100.0%; Pred. No. 8.4e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
 DB 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
 QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLLK 160
 DB 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLLK 160

RESULT 10
 AAG74083
 ID AAG74083 standard; protein; 175 AA.
 AC AAG74083;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:4847.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 22.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US026524.
 XX
 PR 29-SEP-1999; 99US-0157137P.
 PR 03-NOV-1999; 99US-0163280P.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI; 2001-235357/24.
 DR N-PSDB; AAH33514.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers.
 XX
 PS Claim 11; Page 6630-6631; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
 CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922
 XX
 SQ Sequence 175 AA;

Query Match 100.0%; Score 809; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 9.5e-88;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
 DB 16 MSEVRPLSRDILMETLLYEQLLEPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 75
 QY 61 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 120
 DB 76 LACIGDEMDSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLRSFMDGFTTLKENIMR 135
 QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLLK 160
 DB 136 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLLK 175

RESULT 11
 ABP41517
 ID ABP41517 standard; protein; 175 AA.
 AC ABP41517;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HCOMW35, SEQ ID NO:2649.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 22q13.31.
 XX
 OS Homo sapiens.

XX PN WO200200677-A1.
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US018569.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR N-PSDB; ABQ54594.
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX PS Claim 11; SEQ ID NO 2649; 2922pp; English.
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 175 AA;
Query Match 100.0%; Score 809; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.5e-88;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
DB 16 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 75
QY 61 LACIGDEMVDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
DB 76 LACIGDEMVDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 135
QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLK 160
DB 136 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLK 175
RESULT 12

AAE37657
ID AAE37657 standard; protein; 378 AA.
XX AC AAE37657;
XX DT 27-AUG-2003 (first entry)
XX DE Bcl2 related protein #8.
XX KW Bcl2 related protein; growth; protein expression.
XX OS Unidentified.
XX PN WO2003040374-A1.
XX PD 15-MAY-2003.
XX PF 02-NOV-2001; 2001WO-US045553.
XX PR 02-NOV-2001; 2001WO-US045553.
XX PA (CENZ) CENTOCOR INC.
XX PI Lee C, Ly C, Moore G, Shi X;
XX DR WPI; 2003-441576/41.
XX PT New protein expression enhancing Bcl2 related nucleic acid for producing
PT commercially useful amounts of expressed protein, comprises a nucleic
PT acid that encodes an expressible protein or at least one Bcl2 related
PT protein.
XX PS Disclosure; Page 54-55; 64pp; English.
XX CC The invention relates to methods and compositions for enhanced protein
CC expression and/or growth of cultured cells using co-transcription of at
CC least one Bcl2 related protein encoding nucleic acid molecules. The
CC invention is useful in providing enhanced growth of and/or protein
CC production from cultured mammalian host cells used for the production of
CC commercially useful amounts of expressed protein. The present sequence is
CC Bcl2 related protein
XX SQ Sequence 378 AA;
Query Match 100.0%; Score 809; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.7e-87;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
DB 1 MSEVPLSRDILMETLLYEQLLEPPTMEVLGMDTSEEDLDPMEDFDSLECMGSDALALR 60
QY 61 LACIGDEMVDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
DB 61 LACIGDEMVDVSLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLVLSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLLPLLSGGLHLK 160
RESULT 13
ADT77558
ID ADT77558 standard; protein; 160 AA.
XX AC ADT77558;
XX DT 13-JAN-2005 (first entry)
XX DE Ser35Asp Bik.
XX KW Bik; nbk; pro-apoptotic; BH3-only protein; Bcl-2 homology region;
KW BH3 domain; initiator; apoptosis; chromosome 22q; human; breast; colon;

KW cancer; cell proliferation; phosphorylation; protein transduction domain;
KW inhibition; proliferative disorder; hematologic malignancy; sarcoma;
KW leukaemia; lymphoma; myeloma; prostate; ovarian; lung; brain; pancreatic;
KW liver; bladder; gastrointestinal cancer; oestrogen receptor positive;
KW EGF receptor overexpressing; optionally overexpressing Her2/neu-;
KW Akt overexpressing; androgen dependent; restenosis; sensitizing; tumour;
KW chemotherapeutic agent; antitumour activity.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
XX FT Misc-difference 35
XX FT /label= S35D

XX WO2004089981-A2.

XX 21-OCT-2004.

XX 02-APR-2004; 2004WO-US010342.

XX 02-APR-2003; 2003US-0459901P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Hung M, Li Y, Wen Y;

XX WPI; 2004-748724/73.

XX New mutant Bik polypeptides having anti-cell proliferation activity
XX and/or pro-apoptotic activity useful for the treatment of cancer.

XX Claim 5; SEQ ID NO 8; 152pp; English.

XX This sequence represents Ser33Asp Bik. Bik, also known as nbk, is one of
CC the pro-apoptotic BH3-only proteins, which have only one of the Bcl-2
CC homology regions, BH3 domains, and have recently been recognised as
CC essential initiators of apoptosis. Bik is located on chromosome 22q. Loss
CC of informative alleles in this region may be related to the development
CC of human breast and colon cancer. The mutant Bik polypeptides of the
CC invention have anti-cell proliferation activity and/or pro-apoptotic
CC activity. Wild type Bik is mutated at either Thr33, Ser35 or both Thr33
CC and Ser35. These substitutions prevent the phosphorylation of mutant Bik
CC under conditions that would result in phosphorylation of an unsubstituted
CC Bik polypeptide. The mutant Bik polypeptide further comprises a protein
CC transduction domain and is complexed with a lipid. The mutant Bik of the
CC invention is used for inhibiting cell proliferation in the treatment of a
CC sarcoma, leukaemia, lymphoma, myeloma, breast, prostate, ovarian, lung,
CC brain, pancreatic, liver, bladder or gastrointestinal cancer (including
CC oestrogen receptor positive, EGF receptor overexpressing, optionally
CC overexpressing Her2/neu-, Akt overexpressing and optionally androgen
CC dependent cancers)) and restenosis in an animal (such as human); and for
CC sensitizing the tumour cell to a chemotherapeutic agent. The mutant Bik
CC polypeptides exhibit anti-cell proliferation activity and/or pro-
CC apoptotic activity i.e. substantially the same or more effective than the
CC native Bik polypeptides and are capable of exhibiting strong antitumour
CC activity in both in vivo and in vitro cells. The polypeptides sensitize
CC the tumour cell to the chemotherapeutic agent and enhance the
CC chemotherapeutic agent-induced apoptosis of the cells, thus are useful
CC for the treatment of resistant tumours.

XX Sequence 160 AA;

Query Match 99.5%; Score 805; DB 8; Length 160;
Best Local Similarity 99.4%; Pred. No. 2.5e-87;
Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSEVPLSRDILMTLLYEQLLEPTMEVLGWTDSDELDPMEDPDSLECEGSDALALR 60
DB 1 MSEVPLSRDILMTLLYEQLLEPTMEVLGWTDSDELDPMEDPDSLECEGSDALALR 60
QY 61 LACIGDEMDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120

Db 61 LACIGDEMDVSLRAPRLAQLSEVAMHSLGLAFIYDQTEDIRDVLSFMDGFTTLKENIMR 120
QY 121 FWRSPNGSWVSCBOVLALLLLALLLLPLLSGGLHLK 160
Db 121 FWRSPNGSWVSCBOVLALLLLALLLLPLLSGGLHLK 160
RESULT 14
ADT77557
ID ADT77557 standard; protein; 160 AA.
XX
XX AC ADT77557;
XX DT 13-JAN-2005 (first entry)
XX DE Thr33Asp Bik.
XX Bik; nbk; pro-apoptotic; BH3-only protein; Bcl-2 homology region;
KW BH3 domain; initiator; apoptosis; chromosome 22q; human; breast; colon;
KW cancer; cell proliferation; phosphorylation; protein transduction domain;
KW inhibition; proliferative disorder; hematologic malignancy; sarcoma;
KW leukaemia; lymphoma; myeloma; prostate; ovarian; lung; brain; pancreatic;
KW liver; bladder; gastrointestinal cancer; oestrogen receptor positive;
KW EGF receptor overexpressing; optionally overexpressing Her2/neu-;
KW Akt overexpressing; androgen dependent; restenosis; sensitizing; tumour;
KW chemotherapeutic agent; antitumour activity.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 33
XX FT /label= T33D
XX WO2004089981-A2.
XX 21-OCT-2004.
XX 02-APR-2004; 2004WO-US010342.
XX 02-APR-2003; 2003US-0459901P.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Hung M, Li Y, Wen Y;
XX WPI; 2004-748724/73.
XX New mutant Bik polypeptides having anti-cell proliferation activity
XX and/or pro-apoptotic activity useful for the treatment of cancer.
XX Claim 5; SEQ ID NO 7; 152pp; English.
XX This sequence represents Thr33Asp Bik. Bik, also known as nbk, is one of
CC the pro-apoptotic BH3-only proteins, which have only one of the Bcl-2
CC homology regions, BH3 domains, and have recently been recognised as
CC essential initiators of apoptosis. Bik is located on chromosome 22q. Loss
CC of informative alleles in this region may be related to the development
CC of human breast and colon cancer. The mutant Bik polypeptides of the
CC invention have anti-cell proliferation activity and/or pro-apoptotic
CC activity. Wild type Bik is mutated at either Thr33, Ser35 or both Thr33
CC and Ser35. These substitutions prevent the phosphorylation of mutant Bik
CC under conditions that would result in phosphorylation of an unsubstituted
CC Bik polypeptide. The mutant Bik polypeptide further comprises a protein
CC transduction domain and is complexed with a lipid. The mutant Bik of the
CC invention is used for inhibiting cell proliferation in the treatment of a
CC sarcoma, leukaemia, lymphoma, myeloma, breast, prostate, ovarian, lung,
CC brain, pancreatic, liver, bladder or gastrointestinal cancer (including
CC oestrogen receptor positive, EGF receptor overexpressing, optionally
CC overexpressing Her2/neu-, Akt overexpressing and optionally androgen
CC dependent cancers)) and restenosis in an animal (such as human); and for
CC sensitizing the tumour cell to a chemotherapeutic agent. The mutant Bik
CC polypeptides exhibit anti-cell proliferation activity and/or pro-

CC apoptotic activity i.e. substantially the same or more effective than the
CC native Bik polypeptides and are capable of exhibiting strong antitumour
CC activity in both in vivo and in vitro cells. The polypeptides sensitize
CC the tumour cell to the chemotherapeutic agent and enhance the
CC chemotherapeutic agent-induced apoptosis of the cells, thus are useful
CC for the treatment of resistant tumours.
XX
SQ

Query Match 99.3%; Score 803; DB 8; Length 160;
Best Local Similarity 99.4%; Pred. No. 4.4e-87;
Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFSLSCMEGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFSLSCMEGSDALALR 60
QY 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGLHLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGLHLHLK 160

RESULT 15
ADT77559
ID ADT77559 standard; protein; 160 AA.
AC ADT77559;
XX
DT 13-JAN-2005 (first entry)
XX
DE Thr33Asp, Ser35Asp Bik.
XX
KW Bik; nbk; pro-apoptotic; BH3-only protein; Bcl-2 homology region;
KW BH3 domain; initiator; apoptosis; chromosome 22q; human; breast; colon;
KW cancer; cell proliferation; phosphorylation; protein transduction domain;
KW inhibition; proliferative disorder; hematologic malignancy; sarcoma;
KW leukaemia; lymphoma; myeloma; prostate; ovarian; lung; brain; pancreatic;
KW liver; bladder; gastrointestinal cancer; oestrogen receptor positive;
KW EGF receptor overexpressing; optionally overexpressing Her2/neu-;
KW Akt overexpressing; androgen dependent; restenosis; sensitizing; tumour;
KW chemotherapeutic agent; antitumour activity.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 33 /label= T33D
FT FT
FT Misc-difference 35
FT /label= S35D
XX
PN WO2004089981-A2.
XX
XX 21-OCT-2004.
XX
XX 02-APR-2004; 2004WO-US010342.
XX
XX 02-APR-2003; 2003US-0459901P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Hung M, Li Y, Wen Y;
XX
XX WPI; 2004-748724/73.
XX
XX New mutant Bik polypeptides having anti-cell proliferation activity
XX and/or pro-apoptotic activity useful for the treatment of cancer.
XX
XX Claim 5; SEQ ID NO 9; 152pp; English.

CC This sequence represents Thr33Asp, Ser35Asp Bik. Bik, also known as nbk,
CC is one of the pro-apoptotic BH3-only proteins, which have only one of the
CC Bcl-2 homology regions, BH3 domains, and have recently been recognised as
CC essential initiators of apoptosis. Bik is located on chromosome 22q. Loss
CC of informative alleles in this region may be related to the development
CC of human breast and colon cancer. The mutant Bik polypeptides of the
CC invention have anti-cell proliferation activity and/or pro-apoptotic
CC activity. Wild type Bik is mutated at either Thr33, Ser35 or both Thr33
CC and Ser35. These substitutions prevent the phosphorylation of an unsubstituted
CC Bik polypeptide. The mutant Bik polypeptide further comprises a protein
CC transduction domain and is complexed with a lipid. The mutant Bik of the
CC invention is used for inhibiting cell proliferation in the treatment of a
CC proliferative disorder e.g. cancer (such as hematologic malignancies,
CC sarcoma, leukaemia, lymphoma, myeloma, breast, prostate, ovarian, lung,
CC brain, pancreatic, liver, bladder or gastrointestinal cancer (including
CC oestrogen receptor positive, EGF receptor overexpressing, optionally
CC overexpressing Her2/neu-, Akt overexpressing and optionally androgen
CC dependent cancer)) and restenosis in an animal (such as human); and for
CC sensitizing the tumour cell to a chemotherapeutic agent. The mutant Bik
CC polypeptides exhibit anti-cell proliferation activity and/or pro-
CC apoptotic activity i.e. substantially the same or more effective than the
CC native Bik polypeptides and are capable of exhibiting strong antitumour
CC activity in both in vivo and in vitro cells. The polypeptides sensitize
CC the tumour cell to the chemotherapeutic agent and enhance the
CC chemotherapeutic agent-induced apoptosis of the cells, thus are useful
CC for the treatment of resistant tumours.
XX
SQ

Sequence 160 AA;

Query Match 98.8%; Score 799; DB 8; Length 160;
Best Local Similarity 98.8%; Pred. No. 1.3e-86;
Matches 158; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFSLSCMEGSDALALR 60
DB 1 MSEVRPLSRDILMETLLYEQLLEPTMEVLGWTDSSEDLDPMEDFSLSCMEGSDALALR 60
QY 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
DB 61 LACIGDEMDSVLRAPLAQLSEVAMHSLGLAFIYDQTEDIRDLRSFMDGFTTLKENIMR 120
QY 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGLHLHLK 160
DB 121 FWRSPNPGSWVSCQVLLALLLALLPLLSGGLHLHLK 160

Search completed: March 15, 2006, 19:08:55
Job time : 190 secs

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